score and is	Result	1	0 0 3 4 4 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8			13				24 102 C 25 102				2 E 4		37 84 38 84	39	αο α	44 79		RESULT 1	AX268026 LOCUS	ACCESSION	VERSION KEYWORDS	SOURCE	acwagaaaa	AUTHORS TITLE	JOURNAL
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model	<pre>Run on: March 21, 2003, 11:06:57 ; Search time 5315.66 Seconds</pre>	Title: US-09-802-208B-1 Perfect score: 1848 Sequence: 1 atgaacgaacaatttacatgtctacgcgttaattaactaa 1848	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 2054640 seqs, 14551402878 residues	Total number of hits satisfying chosen parameters: 4109280	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	Embl:*	2: gb_htg:* 3: gb_in:*	4: gb_om:* 5: gb_ov:*	6: 9D_pat:* 7: 7	9: qb_pr:* 10: qb_pr:*		13: gb_un.* 14: gb_ui.*			20: em_nu.: 21: em or:*							36: em_htg_mam:* 37: em_htg_vrt:*	38: em_sy:* 39: em_htgo_hum:* 40: em_htgo_mis:*	41:	Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

linear PAT 26-OCT-2001 Escherichia coli.
Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
I Parrott, W., Lafayette, P. and Kane, P.
Arabitol or ribitol as positive selectable markers
Patent: WO 0166779-A 1 13-SEP-2001; DNA AX268026 1848 bp Sequence 1 from Patent W00166779. AX268026 AX268026.1 GI:16516559

Db 901 GGTGTTATTA	Qy 961 CTGAATTGCG/ 	Oy 1021 CTCCAGCTAAC 	Qy 1081 AATACCATGG; 	Oy 1141 GCTCAAACGGG Db 1141 GCTCAAACGGG	Qy 1201 GTGGAAGATA 	Qy 1261 GCGTCGGTAR: 	Oy 1321 ATGGCTGGG 	Oy 1381 TTTATCTATCJ Db 1381 TTTATCTATCJ	Oy 1441 AACGGTATCG, 	Qy 1501 ATTCAGGACA(D) DD 1501 ATTCAGGACA(D)	Qy 1561 GCCCCACAC. Db 1561 GCCCCACAC.	0y 1621 CCTGCACTGT 	Qy 1681 CAGGATGGCA' 		Oy 1801 GCGTTGTTGCC 	AF045245/C AF045245/C LOCUS AF045245	DEFINITION NEESTHEE D-X91ulos ACCESSION AF045245 VERSION AF045245
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 	oli" 	DB 6; Length 184 0; Indels	 AGGTTCTTTTCATCGCGCAC 	 PAAACGCTGGAGCATTGCTG 	 ACTCAGTGCACAGAAAGGTCC 	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ATTGCTGAAGGGGCAGATCO	 5TACTACCTGAATACCAGTC! 	TAAAGGGGGATGCAAAACAA'	NAÁTAACGCCGGACCACTAAK	AGGTTCTTTTCATCGCGCACA 	PAAACGCTGGAGCATTGCTGG	NCTCAGTGCACAGAAAGGTCC 	VTATGAAGAGATCACCTCAA? 	ATTGCTGAAGGGGCAGATCC	TACTACCTGAATACCAGTC/ 	AAAGGGGGATGCAAAACAAT
y of Georgia Research Foun- Location/Qualifiers	1 c	100.0%; Score 1848; 100.0%; Pred: No. 0; tive 0; Mismatches	ATGAACGAACAATTTACATGGCTGCACATCGGGTTAGGTTCTTTCATCGCGCACATCAGATCATLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GCGTGGTATCTACACGGTTTGCAGGTGATGGGGGGGATAAACGCTGGAGCATTGCTGCGGGC HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	AATATTCGTAATGATGCTGAACATGTCGTACAGGCACTCAGTGCACAGAAAGGTCGCTAT	GTGCTGGAAACCGTCAGCCCGGAAGGGGTAAGCGAATÄTGAAGAGTCACTCAATTCAG 	AAGTTGATACCGTGGCAGGCAGATTTACAACCGCTGATTGCTGAAGGGGCAGATCCGAAG		CTGGAAGTTAACAATCCTGATTTAGCGGCAGATCTTAÀAGGGGGATGCAAACAATTTAC 	GGTGTTATTACCCGTATCCTCGAAGCGCGTATGGCAAATAACGCCGGACCACTAACCCTG 	ATGAACGAACAATTTACATGGCTGCACATCGGGTTAGGTTCTTTTCATCGCGCACATCAG 	GCGTGGTATCTACACCGTTTGCAGGTGATGGGCGATAACGCTGGAGCATTGCTGCGGGCGCGTTTGTTGCTGCGGGCGATAACGCTGGAGCATTGCTGCGGGCGATAAACGCTGGAGCATTGCTGCGGGCGATAAACGCTGGAGCATTGCTGCGGGCGATAAACGCTGGAGCGGGGCGATAAACGCTGGAGCGGGCGG	AATATTCGTAATGATGCTGAACATGTCGTACAGGCACTCAGTGCACAGAAAGGTCGCTAT	GTGCTGGAAACCGTCAGCCCGGAAGGGGTAAGCGAATATGAAGAGTCACCTCAATTCAG 	AAGTTGATACCGTGGCAGGCAGATTTACAACCGCTGATGCTGAAGGGGCAGATCCGAAG	ACAAAAGTGATTGCTTTCACCGTCACCGAAGGGGGGGTA ^C TACCTGAATACCAGTCACAA 	CTGGAAGTTAACAATCCTGATTTAGCGGCAGATCTTAAÁGGGGGATGCAAAACAATTTAC
University of Loca	494	/ Match 100.0%; Local Similarity 100.0%; les 1848; Conservative	ATGAACGAACAATTT. 	GCGTGGTATCTACAC 	AATATTCGTAATGAT(GTGCTGGAAACCGTC 	AAGTTGATACCGTGG 	ACAAAAGTGATTGCT' 	CTGGAAGTTAACAAT 	GGTGTTATTACCCGT. 	ATGAACGAACAATTr. 	GCGTGGTATCTACAC 	AATATTCGTAATGAT 	GTGCTGGAAACCGTC 	AAGTTGATACCGTGG 	ACAAAAGTGATTGCT: 	CTGGAAGTTAACAAT(
FEATURES	SOUTCE BASE COUNT	Query Ma Best Loc Matches	Qy 1 Db 1		Qy 121 Db 121	Oy 181 Db 181	Oy 241 Db 241	Qy 301 Db 301	Oy 361 Db 361	Oy 421 Db 421	Oy 481 Db 481	Oy 541 Db 541	Qy 601 Db 601	Qy 661	Qy 721 Db 721	Oy 781 Db 781	Oy 841 o

BCT 30-AUG-2001 5930 bp DNA linear BCT 30-AUG-21 ella pneumoniae D-arabinitol transporter (dalT), lose-kinase (dalK), D-arabinitol dehydrogenase (dalD), and 350 (dalR) genes, complete cds. 15 U97126 ACCAACCAACGCGTCGCTGCGGATGGTTTCTCGAAAATTCCGGCGATGATT 1560 1740 SCAGGTACGTTAATCGGTCAAAATATATCCACGAAAGCACAATGACCGAT 1380 SATITGCCAACCTACCGTGATGTTGTACTCAAGCGTTTTACCAATCCACAT 1500 STGCGAGAGTGCTACCAGCGAGGCGTTCGCCCGAATGCCACCGCCATGTTA 1620 ACTGGCAAACAGGATGTCATCGACTGGCTGAGTACAAATACCACTTGCCCG GTTGACCGCATTACGCCTCCGCAGCAGAACTTCCGGCACGATCAAG CTGCGAGAGTGCTACCAGCGAGGCGTTCGCCCGAATGCCACGCCATGTTA ACTGGCAAACAGGATGTCATCGACTGGCTGAGTACAAATACCACTTGCCCG STTGACCGCATTACGCCTCGTCCGGCAGCAGCATCCGGCACGCATCAAG ATCCCCTATGAAGAGGCGAAGATTCGCATTCTTAACTCTTCACACAGTTGC PTTTACGTATTCATGGAGCAGTGGCATCACGGCAAACTGCCCTATGAATAT ATCCTTGATGCACCAGCTGTCCATGCAATGTTACAGTCTGCCGATCCCGTC SCCAGTGATAAAGCGCTGTTTGGCGATTTAACCGAACGTGAAGATTTTGCC AATTTCCGTGATGTCCGTCCGGCACTGGAGAAGGTCGGTGTCGAACTGGTG GCGAAAAATCGCTGACGTCTACGCGTTAATTAACTAA 1848

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SOURCE

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Pred. No. 6.2e-259;
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46.6%;
Best Local Similarity 76.8%;
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                                                                                                        Heuel,H., Turgut,S., Schmid,K. and Lengeler,J.W. Substrate recognition domains as revealed by active hybrids between the D-arabinitol and ribitol transporters/from Klebsiella
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Heuel,H., Shakeri-Garakani,A., Turgut,S. and Lengeler,J.W.
Genes for D-arabinitol and ribitol catabolism from Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 5930)
Heuel, H. and Turgut, S.
Heuel, H. and Turgut, S.
Burnect Submission
Submitted (29-3AN-1998) Biology, University of Osnabrueck,
Barbarastr. 11, Osnabrueck, NS 49076, Germany
On Reb 23, 1998 this sequence version replaced gi:2735580.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="1033-5p14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (3242.
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="dalT"
complement(421.
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      Klebsiella pneumoniae.
                        pneumoniae
                                                                  Klebsiella.
1 (bases 1 to 5930)
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                          Klebsiella
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                        ORGANISM
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3788 . 6484
Agene-"y20105"
/notce-"residues 6 to 869 of 898 are 46.53 pct identical to
residues 6 to 865 of 879 from E coli K12 : B1381"
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TGYLSKPLLLNLSWQQQQGVLTLTFREGDNQPLARLPWQASANLIQIVNGQWQWPYGQQ
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ERLRGEGWWPKQSLMVFQPLISKDLGIKLRDGTFYAQAAFSAAREQGFTAGGHWVVNN
GGMWLQDGELSGLDFVMSYRLQNHHWQLGAKEPVMLRIASLNNLFDWQNITADLQGTY
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6367. .6675
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GADEDLNOWDALIGDILHSSVWYTLNKGQLTMSNSTHTLVYQOKDWVN"
complement(7530.3379)
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MANFRAGIIGTGKIGVATMRLIKGFGYRLLARÞPYSPEADALELGAEYVDLYLYAESD
VISLHCPMTPENHHLIKNGSFDQMKOGVNI INTSRGGLIDSTRADIDALKQOKIGSLGM
DVYENERDLFFEDKSNDVIQDDVFRRLSSCHNVLFTGHQAFLTFEBALTSISVTLLQNI
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LRVTAAGVITGERTRDARMPLAG
LRVTAAGVITGKLQA VVDAQDISYGGSVNLHLDGQAQAFWDDKGSWQWRVAGSGNLPPLA
ARWDVGGTGSWRDTLITVDTLSTGFDRLQYGLVKVDAPRLILTKPLTWQRDNHHPAFI
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SGKVNGELPLYLNNPQWLVRNGWIANDGMLTIRLDKDLTDSISESNTVAGAAIDMLRY
          t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="residues 20 to 345 of 349 are 81.28 pct identical to residues 1 to 326 of 329 from E. coli K12: B1380; residues 20 to 347 of 349 are 82.31 pct identical to residues 1 to 328 of 329 from GenPept : >emb|CAD01584.1| (AL627270) D-lactate dehydrogenase [Salmonella enterica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6367. 6675
//gene="72006"
/note="residues 39 to 102 of 102 are 58 46 pct identical
to residues 1 to 61 of 61 from E. coli K12 : B1382;
/note="residues 1 to 150 of 150 are 44.73 pct identical residues 1 to 140 of 140 from E. coli K12 : B1379; residues 1 to 160 of 150 are 44.73 pct identical to residues 1 to 140 of 140 from GenPept : spb had56381.11AE005366_7 (AE003366) heat shock protein hslJ [Escherichia coli O157:H7 ED1933]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="fermentative D-lactate|dehydrogenase,
NAD-dependent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'function="enzyme; energy metabolism, carbon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subsp. enterica serovar Typhi]"
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                                                                                                                                                                                              /codon_start=1
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3788. .6484
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3788. KAR
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6367.
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gene

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ERVAMALGILLLSGCVRLEVATPERPITINMNVKIEHBIQIRVDKDVEALLKNGSNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                            6685. .7056
//gene="y2007"
//gene="y2007"
//force="residues 30 to 123 of 123 are 55.31 pct identical
//orce="residues 16 to 109 of 110 from E. coll K12: B1383;
residues 24 to 123 of 123 are 60.00 pct identical
residues 9 to 107 of 107 from GenPept : >9b|AAL20562.1|
//AE080772) putative periplasmic protein [Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="residues 16 to 459 of 467 are 65.09 pct identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGGAAGGGGTAAGCGAATATGAAGAGATCACCTCAATTCAGAAGTTGATACCGTGGCAG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGATTTACAACCGCTGATTGCTGAAGGGGCCAGATCCGAAGACAAAAGTGATTGCTTTC 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCGAAGCGCGTATGGCAAATAACGCCGGACCACTAACCCTGCTGAATTGCGATAACGTG 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499 TGGCTGCACATCGGGTTAGGTTCTTTTCATCGCGCACATCAGGCGTGGTATCTACACCGT 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
residues 50 to 102 of 102 are 68.51 pct identical to residues 10 to 63 of 63 from GenPept : >gb|AAL20563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      559 TTGCAGGTGATGGGCGATAAACGCTGGAGCATTGCTGCGGGCAATATTCGTAATGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8393 AAAGCGCTAGATCATCTGGTAGCGCAAGGGAGTAAACCCGAAACTCGCGTGATCTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATTTAGCGGCAGATCTTAAAGGGGGATGCAAAACAATTTACGGTGTTATTACCCGTATC
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Pred. No. 3.6e-173;
0; Mismatches 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7275. .8678)
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/function="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7275. .8678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVNRAAEGEYVRGINGQWMKR'
                                                                                                                                                                                                                                                                                                                                                                                                            typhimurium LT2]"
                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="y2008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.9%;
Best Local Similarity 64.8%;
Matches 873; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 3
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INSELTZSDGGTEDRGQAMTRWQVEESEPETQRILGSTRTERFVYAANTD
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VLHWESGRPDEITDDQIRXSYDNLAGSCSLELGGDGNIISABEXYRYGGAAVWAVRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Similar to Photorhabdus luminescens insecticidal toxin complex protein TcCC TR:085157 (EMBL:AF047028) (1043 aa) fasta scores: E(): 0, 60.4% id in 695 aa, and to Serratia entomophila plasmid pADAP virulence determinant SepC TR:AAG09644 (EMBL:AF135182) (973 aa) fasta scores: E(): 0, 62.2% id in 875 aa. Similar to YP02380 (984 aa) fasta scores: E(): 0, 64.2% id in 875 aa. Similar to YP02380 (984 aa) fasta scores: E(): 0, 64.3% identity in 773 aa overlap, and to YP03573 (952 aa) fasta scores: E(): 0, 52.1% identity in 729 aa overlap. Note the differing C-terminus of the product of this CDS and the G+C content 56%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFIDRNGLNSELLYSQAFKRTANKYNVIJGVRAPNPIGETLLKEGFPSKNFHMKAKSS
PTGPTAGFIAEDPIYSKVSPSAYKKQRASIDKAKALGSESIDLFISKSRINELIDTGN
LNSLGENRYSAKYPYGTQFFEIGNNGRVLNSEGKPVKVMTNPPEIGERKSNSSPITAD
Parkhill, J., Wren, B.W., Thomson, N.R., Titball, R.W., Holden, M.T.G., Prentice, M.B., Sebaihia, M., James, K.D., Churcher, C., Mungall, K.L., Baker, S., Basham, D., Bentley, S.D., Brooks, K., Cerdeno-Tarraga, A.M., Chillingworth, T., Cronin, A., Davies, R.M., Davis, P., Dougan, G., Feltwell, T., Hamilhi, N., Holroyd, S., Jagels, K., Leather, S., Simmonds, M., Skelton, J., Stevens, K., Wultehead, S., and Barrell, B.G. Genome sequence of Yersinia pestis, the causative agent of plague Nature 413 (6855), 523-527 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Details of Y. pestis sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                        2 (bases 1 to 313050)
Parkhill,J.
Direct Submission
Submitted (04-OCT-2001) Submitted on behalf of the Yersinia sequencing team, Sanger Centre, Wellcome Trust Genome Campus Hinxton, Cambridge CB10 ISA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (URL, http://www.sanger.ac.uk/Projects/Y_pestis/)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             database hits"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pestis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="biovar: Orientalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="No significant
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Yersinia
/strain="C092"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref-"taxon:632"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'DLFAIIQVLISQLMKDP"
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/gene="YPO2313"
3272. .3628
/gene="YPO2313"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="YPO2312"
645, 3260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     645. .3269
/gene="YPO2312"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .313050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 3269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
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PUBMED
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gene
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     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NA linear BCT 06-JUN-2002 genome; segment 12/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yersinia pestis.
Yersinia pestis
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
  CGCCATAATGGTGAACGTTTCCATGATGGCCTGGTTGAGTTTCTCCAGCTAACTGGCAAA 1038
                                                                                                                                                                                                         1158
                                                                                                                                                                                                                                                                                                             1218
                                                                                                                                                                                                                                                                                                                                                          7914
                                                                                                                                                                                                                                                                                                                                                                                                             1219 GATGTCCGTCCGCCACTGGAGGAGGTCGGTGTCGAACTGGTGGCGTCGGTAATCCCCTAT 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                    1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACCGCTACGTGACGGAAGATGTCATTCCTTGGCGGATAACGGTATCGATTTGCCA 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1579 TGCTACCAGCGAGGCGTTCGCCCGAATGCCACCGCCATGTTACCTGCACTGTTTTACGTA 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1639 TTCATGGAGCAGTGGCATCACGGCAAACTGCCCTATGAATATCAGGATGGCATCCTTGAT 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCACCAGCTGTCCATGCAATGTTACAGTCTGCCGATCCCGGTGCTGTTATGCCCAGTGAT 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGCGCTGTTTGGCGATTTAACCGAACGTGAAGATTTTGCCGCGTTGTTGCGCGAAAAA 1818
                                                                                                    CAGGATGTCATCGACTGGCTGAGTACAAATACCACTTGCCCGAATACCATGGTTGACCGC 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTACGCCTCGTCCGCCAGCAGAACTTCCGGCACGGATCAAGGCTCAAACGGGTATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1279 GAAGAGGCGAAGATTCGCATTCTTAACTCTTCACACAGTTGCATCGCCTGGGCAGGTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1519 CGCGTCGCTGCGGATGCTTTCTCGAAAATTCCGGCGATGATTGCCCCCACACTGCGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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Yershina pestis strain C092 complete
AJ414152 AL590842
AJ414152.1 GI:15980308
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/transl_table=11
/product = "hypothetical protein"
/protein_id="CAG91122.1"
/db_xref="G1:15980314"
/db_xref="G1:15980314"
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PCKVFSTLIITTQRGRYMNRTLRNES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SWISS-PROT:Q8ZE65"
/translation="MKTVLTLIVAATLSLFSVAFAADTVVPQTTPTATAPAPAVHNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Similar to Escherichia coli acid shock protein Asr
SW:ASR_ECOLI (P36560) (111 aa) fasta scores: E(): 3.5e-08,
50.0% id in 106 aa"
                                                                                                                                                                                                                                                                                                                                    //orde="one of 4 probable transmembrane helices predicted for YPO2116 by TMHMM2.0" 6008. .6220 /gene="YPO2317"
                                                                               transmembrane helices predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14950 TGGCTGCATATTGGTGCTGCCTTCCATCAGCGAGCCCATCAGGCTTGGTATTTACACCGT 15009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15070 ATCCCACTACTGGACACATTGCGGGCGCACACACGGTGAATATGTCTTGGAAACGGTCACA 15129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15190 AAAGGGCTAGATCATCTGGTAGCGCAAGGGAGTAAACCCGAAACTCGCGTGATCTCTTTC 15249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 TGGCTGCACATCGGGTTAGGTTCTTTTCAFCGCGCACATCAGGCGTGGTATCTACACCGT 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                559 TIGCAGGIGATGGGCGATAAACGCIGGACATIGCIGCGGGCAATATICGTAATGATGCT 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      619 GAACATGTCGTACAGGCACTCAGTGCACAGAAAGGTCGCTATGTGCTGGAAACCGTCAGC 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGGAAGGGGTAAGCGAATATGAAGAGATCACCTCAATTCAGAAGTTGATACCGTGGCAG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKTMHHKKAQKPNTIKNTHKTAPEQKAQAAQKHHKAAHSHKAPTVAPAAK"
6835. .7671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        739 GCAGATTTACAACCGCTGATTGCTGAAGGGGCAGATCCGAAGACAAAAGTGATTGCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="No significant database hits. Doubtful CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 313050;
                                                                                                                                                                                                                 transmembrane helices
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative acid shock protein"
/protein_id="CAC91123.1"
/db_xref="G1:15980315"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 588.6; DB 1;
Pred. No. 7.1e-173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 474;
                                                                           /note="one of 4 probable
for YPO2316 by TMHMM2.0"
complement(5407. .5463)
/gene="YPO2316"
                                                                                                                                                                                                                 /note="one of 4 probable for YPO2316 by TMHMM2.0"
                                                                                                                                                                                                                                                                              complement(5509..5574)
/gene="YPO2316"
          complement(5278. .5343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6205. .6208
/gene="YP02317"
6217. .6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="asr"
6217. .6501
/gene="YPO2318"
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/gene="YPO2318"
                                           /gene="YP02316"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6008. .6220
/gene="YPO2317"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
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64.8%;
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              misc_feature
                                                                                                                                                                                                                                                                                         misc_feature
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Q.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:082E69"
/translation="TLYHVGIDVSKATLDICLLADGLDGKRKTKSLPNGISSAEAVIN
WLVMQKRDPKQARLVMEATGIYHED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SPTREMBL:002E68"
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SYMLYGGSFNDFDGSFTFDDKNPAADKVNVYINTNSVDTNHAERDKHLRGKSFLNVAK
FPQAFFESTEVKKNDFOSYSVIGNLTLMGVTKPYTLESKLTGOGNDPWGGYRAGFEANG
NIKKKDFNITTDLGFASQEYELILSVEGVQVK"
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homologue 2 YceJ SW.C56I_ECOLI (P75925) (188 aa) fasta
scores: E(): 0, 62.6% id in 182|aa, and to Pseudomonas
aeruginosa hypothetical protein PA0422 TR.AAG03811
(EMBL:AE004479) (189 aa) fasta scores: E(): 0, 59.3% id in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:08ZE67"
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/translation="WLLKNTREOFGSTITIAIHWLVALTVYALFALGLWMVTLGYYDGW
YHQAPEIHKSVGCILFAVMLFRVIMPFISPPPKPLSSYNRLTRVSAVLAHLMLYSILF
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LAALKHHFIDGDITLKRMLGRSID"
                                                                                                        /db_xref="SPTREMBL:082E70"
Translation="MPHKLLRGDFSLPFTSPKGKNGMSEDVNMGNLHHFGKTIVNSLN
KETNAEGYAGGKLWHNDEAGNPFSPGFDENDKPIFFLPSGGMFQAKNKSELLGFYSR
LRRSGYTPEHSPIFGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Similar to Escherichia coli hypothetical protein
Ycel SW:YCEL ECOLI (P37904) (191 aa) fasta scores: E(): 0,
85.8 id in 191 aa, and to Pseudomonas aeruginosa
hypothetical protein PA04023 TR:AAG03812 (ENBL:AE004479)
(191 aa) fasta scores: E(): 0, 77.4% id in 190 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                           regions of Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(5122. .5187)
/gene="YPO2316"
/note="one of 4 probable transmembrane helices predicted
for YPO2316 by TMHMM2.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative invertase protein (partial)"
/protein_id="CAC91119.1"
/db_xref="GI:15980311"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"putative exported protein"
/protein_id-"CAC91120.1"
/db_xref-"G1:15980312"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative membrane protein"
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                                                                                                                                                                                                                                                 complement(3732, .3941)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4455. .5033)
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                                                                                                                                                                                                                                                                                                                  complement(3732. .3941)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="YPO2315"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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Gaps

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RBS gene

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complement(600. .1070)
/gene="RSC2043"
/note="RS03608"
complement(600. .1070)
/gene="RSC2043"
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/db_xref-"taxon:305"
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                                                         Ralstonia solanacearum.
Ralstonia solanacearum
Bacteria; Proteobacteria;
 segment 12/19.
AL646068 AL646052
AL646068.1 GI:17429060
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Boucher, C.A.
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                                                                        ORGANISM
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TITLE
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               ACCESSION
VERSION
KEYWORDS
                                                                                                                  REFERENCE
AUTHORS
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                                                                                                                                                                        1039 CAGGATGTCATCGACTGGCTGAGTACAAATACCACTTGCCCGAATACCATGGTTGACCGC 1098
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                                                                                                                                                                                                                                                                                                                                                GATGTCCGTCCGGCACTGGAGAAGGTCGGTGTCGAACTGGTGGCGTCGGTAATCCCCTAT 1278
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Ralstonia solanacearum GMI1000 chromósome, complete sequence;
GATITIAGCGGCAGATCTTAAAGGGGGATGCAAAACAATTTACGGTGTTATTACCCGTATC
             1099 ATTACGCCTCGTCCGCCAGCAGCATCCGGCACGGATCAAGGCTCAAACGGGTATTGCC
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                                                                                                                                16270 ATAAATCGTGTCTCTGCTTGCGTTAGC 16296
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Direct Submission
Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston
Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston
Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie
Moleculaire des Interactions Plantes-Microcrganismes INRA-CNRS,
BR27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean
Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS
118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA
ORGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France,
Laboratoire de Biometrie et Intelligence Artificialle INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire
INRA, BP27, F31326 Castanet-Tolosan Cedex
Christian.Boucher@toulouse.inra.fr
http://sequence.toulouse.inra.fr /codon_start=1
/tenss_tant=1
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VGSRLRARVSLLEMEMLPPLQPSPDAPALTGAQMTWGVTIECEGQARPVCVAESISRR (bases 1 to 200050)

Salanoubat, M., Genin, S., Artiguenave, F., Gouzy, J., Mangenot, S., Arlat, M., Billault, A., Brottier, P., Camus, J.C., Cattolico, L., Chandler, M., Choisne, N., Claudel-Renard, C., Cunnac, S., Demange, N., Gaspin, C., Lavie, M., Moisan, A., Robert, C., Saurin, W., Schiex, T., Siguier, P., Thebault, P., Whalen, M., Wincker, P., Levy, M., Weissenbach, J. and Boucher, C.A.

Genome sequence of the plant pathogen Ralstonia solanacearum Unpublished complement (85..573)
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/gene="RSc2042"
/function="miscellaneous; hypothetical/global homology"
/note="Product confidence: hypothetical
gene name confidence: hypothetical
predicted by Codon_usage
predicted by Homology /function="miscellaneous; hypothetical/global homology" /note="product confidence : hypothetical Gene name confidence : hypothetical predicted by Codon_usage beta subdivision; Ralstonia group; /evidence=not_experimental /transl_table=11 /product="CONSERVED HYPOTHETICAL PROTEIN" /organism="Ralstonia solanacearum'

gene

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //function.misscellaneous; hypothetical/global homology"
//functionalisticallaneous; probable
/note="product confidence: probable
Gene name confidence: hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="miscellaneous; hypothetical/global homology"
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Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="CONSERVED HYPOTHETICAL PROTEIN"
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Pred. No. 2.3e-117;
0; Mismatches 568;
                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental/transl_table=11
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                                                                                                                                                    /gene="RSc2047"
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illarity 57.3%;
Conservative
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794
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                                                                                                                                                                                                                                                                     1455 GCCAACCTACCGTGATGTTGTACTCAAGCGTTTTACCAATCCACATATTCAGGACACCAA
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                                                                                                                           TCCTGATTTAGCGGCAGATCTTAAAGGGGGATGCAAAACAATTTACGGTGTTATTACCCG
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KDLPASYDLDDVFPSVRDGLSVKGSLYALPFYAESSITYYRTDLFKDAGLSMPEHPTW
                                                                                                                                                  Pseudomonas fluorescens mannitol operon, MtlE (mtlE), MtlF (mtlF), MtlK (mtlK), mannitol dehydrogenase (mtlD), xylulose kinase (mtlY) and fructokinase (mtlZ) genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erunker, P., Altenbuchner, J. and Mattes, R.
Brunker, P., Altenbuchner, J. and Mattes, R.
Structure and function of the genes involved in mannitol, arabitol and glucitol utilization from Pseudomonas fluorescens DSM50106 Gene 206 (1), 117-126 (1998)
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                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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subunit of the periplasmic binding protein dependent
mannitol transport system"
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Bunker, P., Altenbuchner, J., Kulbe, K.D. and Mattes, R.
Cloning, nucleotide sequence and expression of a mannitol
dehydrogenase gene from Pseudomonas fluorescens DSM 50106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 10031)
Bruenker, P., Altenbuchner, J. and Mattes, R.

Bruenker, Submission
Submitsed (10-JUN-1997) Institute of Industrial Genetics,
University of Suttgart, Allmandring 31, Stuttgart 70569,
On Aug 4, 1997 this sequence version replaced 91:2065484.

Location/Qualifiers
                                                                                                                                BCT
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QLTRVQIDAWLGFAIRAAALTGGKTGPDLPYRQQLG"
1 3194 c 2919 g 1877 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                /function="ATP dependent phosphorylation of fructose, glucose and glucitol" /note="Mtl2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    565 GIGAIGGGCGATAAAC---GCIGGAGCAIIGCIGCGGGCAATAIICGIAAIGAIGCIGAA
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8423. .9361
/gene="mtlZ"
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SAVTLGIRPEHLEIASPGQTTLIVYTADVGERĻGSDTFCHVITSNGEPLTMRIRGDMAS
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WEKVGVQFTDDVTPYEEMKIGLLNGSHLALTYLGFLKGYRFVHETMNDPLFVAYMRAY
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4136. 5239
4136. 5239
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5258. ...
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1033 GGCAAACAGGATGTCATCGACTGGGTACAAATACCACTGCCCGAATACCATGGTT 1092 11 1 1 1 1 1 1 1 1	1333 GGTACGTTAATCGGTCAAAATATATCCACGAAAGCACAATGACCGATTTTATCTATC	PESULT 7 AP003003 AP003003 AP003003 BESULT 7 AP003003 AP003003 AP003003 BESULT 7 AP003003 BEFINITION AP003003 AP00	URL:http://www.kazusa.or.jp/rhizobase/, URL:http://www.kazusa.or.jp/rhizobase/, Tel:81-438-52-3936(ex.2338), Fax:81-438-52-3934) Tel:81-438-52-3936(ex.2338), Fax:81-438-52-3934) FEATURES Location/Qualifiers Location/Qualifiers 1

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Matches 524;
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Best Local S
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PGYLMQLLVEMDGFESNESIILIAAATRRPDVLDPALLRPGRFPDRQVVVPNPDIYGREK
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contains similarity to cell cycle protein MesJ/cytosine
                                                                                                    HNPYYDNGIKLFGPDGYKLSDEIEERIESMLDKDVELTLADSDGLGRAKRVDGVHDRY
                                                                                                                                                                                                                               KAAIEDARNRLGKAGRLVIRPSGTEPLIRVMAEGDDPQLVEAVVNDIVEVISETRSAA
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QAFENLGLPQGEPRLPVFAARPVVSPFARFLPSFDLAPARAVAELIGASPLPASPLGG
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Pred. No. 3.5
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                                                                                                                                                                                                      complement(12098. .13210)
                                                                                                                                                                                                                                                                                                                                        /note="unknown protein".
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DINESDGRPPWELVGVQVYVNDSYELMKILLIAGGHSAMGYTGYLAGYTYIHEVVNDP
DINEYIRKYIRKEBY PLLPKVPODFEEYIASVLERESNPAIQDTVARICLMGSGKMP
KYVLPSIYEQLRKPDGKYKLLAVCVAGWFRYLTGVDMGKPFEIEDPMAPTLRAAAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mtkSDeftTaTSLNAKTLKSFESTLPIPTYPREGVKGGIVHLGVG
AFRESHLAFORPHRLMOMSICCOKJLMKADALMRDAMKADOLTTLJERGITKDT
NAYIVGSITAYRVABDDPRAVIEKMANPDTHIVSLTVTENGYYHSEATNSLMTDAPEI
INDLNHPEKPDTLYGYLYEALLLRYKRGLTPFTIMSCDNMPQNCVTVKTMLVARANLA
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                                                         132971 GGGTGGTCGAAGACAATTTCTCCCCGGCAGGCCGGACTGGGAAAAGTTCGGCGTCACCA 133030
                                                                                                                                            TGGTTGGCGATGTCGGCCCCTTCGAGGACATGAAGCTCAGGCTGCTCAACGGCGCGCATT 133090
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 3250)
Andre, B., Iraqui Houssaini, I., Urrestarazu, L.A. and Vissers, S.
Unpublished
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Submitted (29-ARR-1996) Data collected by MIPS on behalf of the Submitted (29-ARR-1996) Data collected by MIPS on the Buropean yeast chromosome XIV sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG: E-mail: Mewes@mips.embnet.org
                    GGGTCGTGGAAGATAATTTCCGTGATGTCCGTCCGGCACTGGAGAAGGTCGGTGTCGAAC 1255
                                                                                                      TGGTGGCGTCGGTAATCCCCTATGAAGAGGCGAAGATTCGCCATTCTTAACTCTTCACACA 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                               CACATATTCAGGACACCAACCAACGGGTCGCTGCGGATGGTTTCTCGAAAATTCCGGGGA 1555
                                                                                                                                                                                                                                133091 CGGGCATCGCCTATCTCGGCCTGCTCAGCGGCCACGCCACCGTCGACCGCGCCTTTGCCG
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                                                                                                                                                                                        GTTGCATCGCCTGGGCAGGTACGTTAATCGGTCAAAATATATCCACGAAAGCACAATGA
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Unpublished
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S.cerevisiae chromosome XIV reading frame ORF YNR073c.
Z71688 Y13139
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/db_xref="taxon:4932"
/chromosome="X1V"
/complement(441, .1949)
/note="ORF YNR073c"
/codon_start=1
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/db_xref="SWISS-PROT:P39941"
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Unpublished
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Saccharomyces cerevisiae
Eukaryota: Fungi; Ascomycota: Saccharomycotina; Saccharomycetales; Saccharomycetales; Saccharomycetales
                                                               Length 3250,
                                                                                                                Indels
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Andre, B., Iraqui Houssaini, I., Urrestarazu, L.A.
                                                                                                                0; Mismatches 315;
                                                                  Score 113; DB 8;
Pred. No. 1.6e-23;
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651 c
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326 GTCAACGACCCAACTATCAACAAGTATATCCGTGTTTTGATGCGTGAGGAAGTTATCCCA 267
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/chromosome="XIV"
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TINXITRVLAKEEVIPLLAKPKVGVDFEEYTAGYLERESNPATQDTVARTCLMGSGKMP
KYVLPSITEQLKKPGKKLLAVCVAGWFRYLTGVDMNGKPFEIEDP"
COMPLEMENT (2618. .3754)
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VRATGOVTNFRYHGIVKRDNWYDVITRNVISSLQEGTEASIVDADCLETGHAPSGVS
LGPNAGFGOFPLPLLGTINIPSFLISRAKSKNIFSDKMEPLFKK"
1036 c 900 g 1464 t
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KDEKFAAMIEDKVTSPNSMVDRVTPRCTDKERKYVADTWGIKDQCPVVAEPFIQWVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MTINTKNIVVVGAGVFGVSVANHLYRELGGTYAIKLVTASNYVY
FLPSAVRLTVSKDYTKSILPLKNVLDSGIEVIKDTAASFDDKEVVLGSDRAIKFDILV
LATGSKWADPIGSTYTFGDNYKEYFEREASRISDADHILFLGGGFVNCELAGELLFKY
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                                                                                                                                                                                                                                                                   /translation="MTKSDETTATSLNAKTLKSFESTLPIPTYPREGVKGGIVHLGVG
AFHRSHLAVFMHRLMQEHHLKDWSICGVGLMKADALMRDAMKAQDCLYTLVERGIKDT
                                                                                                                                                                                                                                                                                                      NAY IVGSITAYMYAPDDPRAVIEKMANPDTHIVSLTVTENGYYHSEATNSLMTDAPEI
Submitted (29-APR-1996) Data collected by MIPS on behalf of the European yeast chromosome XIV sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsiled, FRG; E-mail: Mewes@mips.embnet.org
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Pred. No. 1.7e-23; '
0; Mismatches 315;; Indels
                                                                                                          cerevisiae"
                                                                                                                                                                                                             /protein_id="CAA96358.1"
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/db_xref="GI:1302612"
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                                                                                                        /organism="Saccharomyces/db_xref="taxon:4932"
                                                                                                                                                            complement(<1. .1316)
/note="ORF YNR073c"
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INDLANPEKPDTLYGYLYEALLLRYKRGLTPPTIMSCDNMPQNGVTVKTMLVAFAKLK
KDEKFRAMIEDKYTSPNSMVDRVTPRCTDKERKYVADTWGIKDOCPVVAEPFIOWVLE
DNESDGRPPWELVGVQVVKVDSYELMKLRLLNGGHSAMGYLGYLAGYTYIHEVVNDP
TINKYIRVLAKREEVIPLLPKYDGYDFEEYTASVLERFSNPAIODTVARICLAMGSGKMP
KYVLPSIYEQLRKPDGKYKLLAVCVAGWFRYLTGVDMNGKPFEIEDP"
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Flpsavrlyvskdytksliplknvldsgievirdhaaspobskevugsbraikeplidv
Latgskwadpigstytpgdnykeyferrestisdabililfgggfvncelagellfky
Lebirsgkrrsiilhasdklidpsglyndtlknvydylskngitlylnydasldts
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 9172)
                                                                                                                      TTTACCAATCCACATATTCAGGACACCAACCAACGCGTCGCTGCGGATGGTTTCTCGAAA 1545
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                                266 TTATTGCCTAAAGTGCCAGGTGTTGATTTCGAAGAGTACACTGCATCAGTGTTGGAAAGA
TGCTTG----GGCGATAACGGTATCGATTTGCCAACCTACCGTGATGTTGTACTCAAGCGT
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Submitted (02-MAY-1995) J.M. Nicaud, Institut National
Recherche Agron., Genetique Moleculaire et Cellulaire,
Thiverval-Grignon, F- 78850 Thiveral Grignon, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  >C>ZBUC14 9172 bp DNA linear S.cerevisiae N3810, N3815, N3820 and N3825 genes. X86790
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/db_xref="GI:805056"
/db_xref="SWISS-PROT:P39941"
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                                                                                                                                                                                                                                                1546 ATTCCGGCGATGATTGCCCCCACACTGCGAGAG 1578
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/gene="N3810"
complement(<1. .1316)
/gene="N3810"
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11743193
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REFERENCE
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                                                            à
                                                                                                                                                                                                                  /translation="MGEBIRLLSSKGLETHSSFCLPEDIFRNRLTWLCSEIRNSGFWI
WSLSWLPLAVWWGMASTWFYPLLTSVVLILALIAILEVVQIOYSKYTLSNQLTQLSKE
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QNEDPRESSEILVPYTEDAVQVYFFKVNAQWRLIHGKRECKLTMLENVKLPKETYRC
KLAWSCQRIRISFSPLDFLPDMSDFFTCANLSPACLVSYWLIDIFFRNIDDFCONIRK
SMKVDDKMQYLSDIINEGGASPEKWDTIARKTNTRLFEKRVWKNEEFFFDGTDCQAFF
PRRIFLGEGSSKYIDADLIYRGVGISPNVPVNSISDLCDKKGFIQVEKNFRVKAVEAG
NVFAIGDVTNFRYHGLVKRDNWVDVLTRNVISSLQEGTEASLVDADCLETGHAPSGVS
LGPNAGFGQFPLPLLGTINIPSFLISRAKSKNLFSDKMEPLFKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MVKLTSIAAGVAAIAATASATTTLAQSDERVNLVELGVYVSDIR
RHAQYYMRQAAHPTETYPVEVAEAVPNYGDFTTMLTGIAPDQVTRMITGVPMYSTRL
RASISKALSKDGIYIIAN"
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Pred. No. 2e-23;
0; Mismatches | 315; Indels
                                                                                                                                                                                                      /db_xref="SWISS-PROT:P52924""
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                                                                                                                                                                                                                                                                                                                                                            6940. 7302
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6940. 7302
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/4938. FARE
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                                                                                                4938. .6062
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Best Local Similarity 49.8%;
Matches 315; Conservative (
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Best Local Similarity
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Wood, D.W., Setubal, J.C., Kaul, R., Okura, V.K., Almeida Jr., N.F.,
Chon, Y., Bovee Sr., D., Chapman, P., Clendenning, J., Deatherage, G.,
Gillet, W., Grant, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M.,
MCClalland, E., Palmieri, A., Raymond, C., Rouse, G.,
Saenphimmachak, C., Wu, Z., Gordon, D., Elsen, J.A., Paulsen, I.,
Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M.,
Krespan, W., Derry, M., Gordon, Kamm, B., Liao, L., Kim, S., Hendrick, C.,
Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.
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PKTVFGFIVAGLKARRDKDLQPFTVMSCDNIFHNGKVTKNAVVGLAALSDPAFANWIS
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Submitted (27-SEP-2001) Department of Microbiology, University of
Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
98195-7242, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobacterium tumefaciens str. C58 (U. Washington).
Agrobacterium tumefaciens str. C58 (U. Washington)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"mannitol 2-dehydrogenase"
/protein_id="AAL45245.1"
/db_xref="GI:17742929"
                                                                                                                                                   ATTCCGCCGATGATTGCCCCCACACTGCGAGAG 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11164 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumefaciens C58
Science 294 (5550), 2317-2323 (2001)
21608550
                                                                                                                                                                                                                                                ATGCCTAAGTATGTTTTGCCATCAATTTACGAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobacterium tumefaciens str. Coof 187 of the complete sequence. AE009374 AE008689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE009374.1 GI:17742928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="mtlK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="mtlK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .1578
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CDS

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GYLLGREFFFFAAMRFRSPADARLFRVKHRTTVFMAGLVIAAFLAVPFLNLLTPLFAA
SLMVHLHKAVSRRDPSFAAGGTEQLRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"endonuclease III"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MNANIMLNEDITPIGSDYDTVRGVIELLTLDYREQPSLEAIAAR
LGQSPTQLQKTFTRWAGLSPKAFLQAVTLDHAKRLLREEDLPLLETSIEVGMSGPGRL
HDLFVTHEAMSPGEWKAKGGGLTIRYGFHASPFGLALVMITDRGLAGCAFADPGDERA
                                                                                                                                                                                                                                                                             IYFALPWIDTLIPGVPDWAGWLSFVFAIFAGIGLALALALLISPVTAVIAGLFLDDVA
DVVEKQNYPDDPPGKAMPIGEAVLSSIKFFGVVIAGNLVALLLLLVPGVNLIAFFLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDNEGGEVPRTREELVTLPGVGRRTANVVMSMAPGVPTLAVDTHVFRIANRLCLAPGK
TTDEVEDRLVRIIPEQYLFHAHHWLILHGRYCCKARKPECERCVIADICKSPEKTFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MDTLNDQPIFAAELVPHRSLGRRGFRLLLILTGFACLIYGGFFL
ATGAWPIGLFFGLDFLLLYIAFRANYRAAKAREEVSVSRTNLSIRKFSPAGRAVEYRF
NPFWARFRVRRHDEIGIVSMHVTGEGRATDIGSFLNPDDRESFAKAFGGALATVRRRM
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KIPMGRAVTYSNIACDIGQPTASRAVGAAVGANPVSFVVPCHRAVGKSGALTGYHWGL
                                                                                                                                                                                                                                                    /translation="MIFDAARLAFGNLFAAETRSVFWKVLGLTLLVLAALWFAIRSIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Atu4457"
complement(5869. .6579)
/gene="Atu4457"
/note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //oce="identified by sequence similarity; putative; ORF located using Blastx/Glimmer" /codon_start=1 /transl_table=11
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located using Blastx/Glimmer"
                                                              /note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424 GATACCCAGGCCATCATCGATACGCTTGCCGATCCGAAAATCCGCATCGTTTCGATGACG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="6-O-methylguanine-DNA methyltransferase"
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                                                                                                                                                            /product."conserved hypothetical protein"
/protein_id="AAL45250.1"
/db_xref="GI:17742934"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"conserved hypothetical protein"
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/db_xref="GI:17742936"
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Pred. No. 4.2e-23;
0; Mismatches 435,
                                                                                                                                                                                                                                                                                                                                                                                            complement(5869. .6579)
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/transl_table=11
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7438. .8310
/gene="ada"
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/gene="Atu4458"
6689. .7171
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8375. .8599
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415; Conserv
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PROCIVIEDSPAGIAAAKAAGMGVFAFTGGSHARFPAFREKIAGLGADAVFDAMPDLV
QLVGSYVGRGGFDGQVERDAG"
2359. 3936
/gene="Atu4453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MMRONLVAVDVGTASARAGIFDPAGKLLARSIHPILMORPRENH
ABEDSTDINANVCIAVRALADAGVLEQSIAALIGEPANTCSLVUTBERGEPVSYSTTDD
DRFDTIVWLDHRAIGEADRITASGHRVLDFAGNSVSPEMONRKLAWIKTHMOSWSRN
SFAFDLADFLIWKATGSAQRSNCTQTAKWNFLAQEHPGWQADYLAFAGLDDIKERAGL
BETTVMRGGAAGDLSPEAAABELGLDFGCOVAAAGNIDAYAGALGALGGCLABUVKHYA
LIAGTSSCLVAMSTOPMPGRSLWGPYWQAVLPGHWLVEGGGSATGALLDHIVRHAAG
GEPDTALHARIVARYTELRELGEAFADRLHVLPDFHGNSPLADPHAVGVVSGLTLD
GKRIVVPATADAVLLGTAMFATAGAGHVLDAMERFCYAVETHVTGGHVKNPLLMELTADVT
GKRIVVPATADAVLLGTAMFATAGAGHVLAASAGAAAGAAMYPGNAFEN
YRRFLAMYRHRQELESL"
ENVAFPNSNVDRITPATGERERNIARDDFGIEDNWPVFCEEFKQWVMEDNFPACRPAL
EEKACVGYKKDVAPYEHMKIRILNGGHAAIAYPAALLDIHYHEAMEHPLIRAFLAKLE
KDEIIPVIPPVPDTDLMDYFCLIERRFLNPKIGDTIPRLAQDGSNRQPKFILESTLDR
LSRGEDIYGLSLVSALMCRYFYGTSDSGKEIVFNDASAERLQAAAIKAKDDPVAFLAL
DDIFGEVAESALFRKRFSHALITLWQBGTAKTĻQLYLDDKLAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"transcriptional regulator, RpiR family"
Protein_id="AAL45248:1"
/db_xref="GI:1742932"
/translation="MVEKLLLNLTRAMKAGTP$ERXIAKYLIEHLDELPFETAQTLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLSLSPWTVGRFLRSLGYRQFSDIRADLRHARETVGADOPVTARGGERHSNPFSQLLS
QQAAQTAPDWTTQTIWRLAMNETTSADDVCLATSPBGLDAGRHFYGRLLECRGHIH
YLGSDNAATVALWDYDPARTLLVINDGGGULLPLQRLSTTARKGGYRTLLTTRFYEW
GPESVDLCLAMPQSORGQGLLQLVSLLEFTLCALSAGADAGKARVRNLAALKRSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MNGDAFARPCKRANHDLTVETSFPGHVLHRTGMRIIVDGLLYFRAHFYSREIPFAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer"
                                                                                                                                                                                                                                                         similarity; putative; ORF
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                                                                                                                                                                                                                                              //octe="identified by sequence
located using Blastx/Glimmer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    located using Blastx/Glimmer'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="ribitol kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAL45247.1"
/db_xref="GI:17742931"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4041. .4874)
/gene="Atu4454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(4041. .4874)
/gene="Atu4454"
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/transl_table=11
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1585. .2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2359. .3936
/gene="Atu4453"
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4897. .5067
                                                                                                                                                                                                                     /gene="Atu4452"
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/gene="Atu4455"
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linear chromosome, section 44 of
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                                                                                                                                                                                                                                                                                                                                                                           1156 GCCGATAAAGCGCCGGTAATGGGCGAAACCTTTATCCAGTGGGGTCGTGGAAGATAATTTC 1215
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Hinkle,G., Slater,S.C. and Goodner,B.
Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Gall
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                                                              915
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   861
 GTCACCGAAGGCGGGTACTACCTGAATACCAGTCACAAACTGGAAGTTAACAATCCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                         1216 CGTGATGTCCGTCCGCCACTGCAGAAGGTCGGTGCTCGAACTGCTGGTGGTGGTAATCCCC
                                                                              664 ATTCCCCACAATGGCAAGGTGACGAAAAACGCGGTGGTCGGGCTGGCAGCGCTCTC---C
                                                                                                                                                                                                                                                   1036 AAACAGGATGTCATCGACTGGCTGAGTACAAATACCACTTGCCCGAATACCATGGTTGAC
                                                                                                                                                                                                                                                                                                                                            781 CGCATCACCCCGCCACCGGGGGGGGGGGAACGCAATATCGCCCGTGACGATTTCGGCATC
                                                                                                                                                                                                                                                                                                                                                                                                1276 TATGAAGAGGCGAAGATTCGCATTCTTAACTCTTCACACAGATGCATCGCCTGGGCAGGT
                                                                                                                          916 ATCCTCGAAGCGCGTATGGCAAATAACGCCGGACCACHAACCCTGCTGAATTGCGATAAC
                                                                                                                                                        604 GGGCTGAAGGCGCGCGCGATAAGGACCTGCAGCCCTTCACCGTCATGTCCTGCGACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      901 CCCGCAGGCCGTCCGGCGCTCGAGAAGCGGGCGTCCAGTTCGTCGAGGATGTTGCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 ATTACCGAGGCGGTTATTTCATCGATGCCTCCGGCTCCTTCAATCCGCAGCATCCGGCC
                                                            TTAGCGCCAGATCTTAAAGGGGGATGC - - - - - AAAACAATTTACGGTGTTATTACCCGT
                                                                                                                                                                                     976 GTGCGCCATAATGGTGAACGTTTCCATGATGGCCTGGTTGAGTTTCTCCAGCTAACTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agrobacterium tumefaciens str. C58 (cereon).
Agrobacterium tumefaciens str. C58 (cereon)
Bacteria; Proteobacteria; alpha subdivision;
Rhizobiaceae; Rhizobium.
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187 of the complete sequence.
AE008240 AE007870
AE008240.1 GI:1515R76A
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ORGANISM
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/db_xref="G1:1515877.1"
/translation="WinDoddery Rapalder Control Control
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TPARADAVKRAVAMGRKQGGSDAVVAAVADRLAISVGAALAGLVPGRVSTFVDADLS
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QAQAIACAEKARFLISFFVGRILDWYKKSTGETYTAFTDFGVVSVRSITNYKANGIG
TVVWGASFRNVGEIEALAGCDRLTISPALLEELDKDNGKLERKLSPDNVKAEALQSLD
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RENCKVYSLLGGIVANUQTNPLDYTWRLASALGAECWFLAPLLUSVSFTRRALIEK
CGLATLY DALALLAIVSCGOLGPHSTSLSEGFISRETLRELVDAGCVCDTWRNFID
AEGRSVDHPINORAMALDLOTLRKAKHIVLASGGAHRAIAIRATIKRIGCNTLITDEA
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GISRSTVIRLLDEAMKRSEVQIWINEGIEDFVSLAGOLEAAYGLDEAVIIPSPGPSPA
2 (bases I to 14945)
Hinkle,G., Slater,S.C. and Goodner,B.
Direct Submission
Submitted (14-AUG-2001) Bioinformatics, Cereon Genomics, 45 Sidney
Street, Cambridge, MA 02139, USA
Approximately 800 bp of telomeric sequence missing from the left
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSCRIPTIONAL REGULATOR IN GLPC-AIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Cereon)
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/gene="AGR_L_812"
/note="transaldolase PA2796 (imported) - Pseudomonas
                                                                                                                                                                                                                                                                                                        end of the chromosome and 200 bp missing from the right end.
Location/Qualifiers
1. 14945
/organism="Agrobacterium tumefaciens str. C58 (Cere/Strain="C58"
/db_xref="taxon:181661"
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2133. .3164
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/note="(AP001509) transcriptional regulator"
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/codon_start=1
/transl_table=11
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complement(3161. .3448)
/gene="AGR_L_815"
/note="Norm-relations"/
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/db_xref="GI:15158763"
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complement/fr
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98. .865
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KLSLSPWTVGRFLRSLGYRQFSDIRADLRHAEETVGADOPVTAEGGERHSNPFSQLLS
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LIAGTSSCLVAMSTQPMPGRSLWGPYWQAVLPCHWLVBGGQSATGALLDHIVRMHAAG
GEPDTALHARIVARVTELRELEGEAFADRLHVLPDFHGNRSPLADPHAVGVVSGLTLD
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GYLLGREFFFFAAMRFRSPADARLFRVKHRTTVFMAGLVIAAFLAVPFLNLLTPLFAA
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DRFDTIVWLDHRAIGEADRLTASGHRVLDFAGNSVSPEWQMPKLWMLKTHWPQSWSRM
SFAFDLADFLTWKATGSAQRSNCTQTAKWNFLAQEHPGWQADYLAFAGLDDLKERAGL
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GKRIVVPATADAVLLGTAMTAATAGGVHASLAAAGAAMYPGNAEISGNPALAAHYERD
IYFALPWIDTLIPGVPDWAGWLSFVFAIFAGIGLALALLISPVTAVIAGLFLDDVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="D-ribulokinase (EC 2.7.1.47)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 112; DB 1;
Pred. No. 4.5e-23;
                                                                    SLMVHLHKAVSRRDPSFAAGGTEQLRG"
                                                                                                                                                                                    /note="hypothetical protein"
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complement(8117. .9694)
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7179. .8017
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48.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="G1:15158768"
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IGHIKTIGIKTRNAKNIALAGMLIDHRGGEVPRTREELTLEGVGRKTANVWSMAF
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TRRRAMLGWETGKA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="06-methylguanine-DNA methyltransferase PA2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (imported) - Pseudomonas aeruginosa (strain PAO1)"
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                                                                                                                                        /gene="AGR_L_816"
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L_816"
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complement(4882, 5364)
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complement(3454. .3690)
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complement(6146. .6883)
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/gene="AGR_L_820"
5402. .6181
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Jia,Y. and Cherry,J.M.
Direct Submission
Submission (04-WAR-1997) Department of Genetics, School of Medicine,
Saccharomyces Genome Database, Stanford University, CA 94305-5120,
                                                                                                                                                                  of Medicine,
94305-5120,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         end of this sequence overlaps with GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.4 KD protein in cerevisiae, Swissprot
                                                                                                  6 (bases 1 to 50849)
Jia,Y. and Cherry,J.M.
Direct Submission
Submitted (12-JUN-1997) Department of Genetics, School Saccharomyces Genome Database, Stanford University, CA
                                                                                                                                                                                                                                                                                                                                                     Saccharomyces Genome Database
URL: http://genome-www.stanford.edu/
e-mall: yeast-curator@genome.stanford.edu
                                                                                                                                                                                                                                                                      Stanford DNA Sequence & Technology Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4932"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1708. .2637)
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complement(join(1708. .1845,2125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to hypothetical subtelomeric Y' repeat from S.
                                                                                                                                                                                                                                                                                         855 California Avenue
Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="YEL076c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing:
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AUTHORS
TITLE
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                                                                                                                                                                                                                               COMMENT
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Saccharomyces cerevisiae.

Bukaryota: Fungi; Ascomycota: Saccharomycetes;
Saccharomycetales; Saccharomycetaces;
Saccharomycetales; Saccharomycetaces;
Saccharomycetales; Saccharomycetaces;
Saccharomycetales; Saccharomycets.

1 (bases 1 to 50849)

Detrior, F.S., Mulligan, J., Hennesy, K., Yelton, M.A., Allen, E., Araujo, R., Aviles, E., Berno, A., Breinan, T., Carpenter, J., Chen, E., Cherry, J.M., Chung, E., Duncan, M., Guzman, E., Hartzell, G., Hunicke-Smith, S., Hyman, R.W., Kayser, A., Komp, C., Lashkari, D., Lew, H., Lin, D., Mosdale, D., Nakhara, K., Namath, A., Norgren, R., Oefner, P., Oh, C., Petel, F.X., Roberts, D., Schl, P., Schramm, S., Shogren, T., Smith, V., Taylor, P., Wei, Y., Botstein, D. and Davis, R.W. The nucleotide sequence of Saccharomyces cerevisiae chromosome V. B. 1313264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae chromosome V cosmids 9669, 8334, 8199, and 11805, 900092
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The sequence of S. cerevisiae cosmids 9669, 8334, 8199, and lambda
                                                                                                                                                                                                                                                                        Palo
                                                                                                    Stanford University, Palo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11212 GAGGATAATTGGCCGGTCTTCTGCGAAGAGTTCAAGCAATGGGTGATGGAGGATAATTTC 11153
1156 GCCGATAAAGCGCCGGTAATGGGCGAAACCTTTATCCAGTGGGTCGTGGAAGATAATTC 1215
                                                                                                                                                                                                                                                1395
                                                                                                                                                                                                                                                                                                                                 1452
                                                                                                                                                                                                                                                                                                                                                                                                                  1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1513 AACCAACGCGTCGCTGCGGATGGTTTCTCGAAAATTCCGGCGATGATTGCCCCCACACTG 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stanford University,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        10912 CTCAACGACTATTTCGGGCTGATCGACGCGCGTTTCCTCAACCCGAAGATTGGCGATACC
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                                                                                                                                                               TATGAAGAGGCGAAGATTCGCATTCTTAACTCTTCACACAGTTGCATCGCCTGGGCAGGT
                                                                                                                                                                                                                                                1453 TTGCCAACCTACCGTGATGTTGTACTCAAGCGTTTTAGCAATCCACATATTCAGGACACC
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5 (bases 1 to 50849)
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Alto, CA 94305-5120
4 (bases 1 to 50849)
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LGDILHIILRACALNFGAGPRGGAGDEBDRSITNEEPIIPSVDEHGLKVCKLRSPNTP
RRLRKTLDAVKALLVSSCACTARDLDIFDDNNGYAMWKWIKILYHEVAQETTIKDSYR
ITLVPSSDGISVCGKLWGELNNCFHMPASFCVIËKFCSENRSEELTSIWKTILFFK"
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EROSWHLKQRYDHHVCLKGLYRPGNLVRLQQTSGTFLHFSRP"
complement(2868. 3236)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /traislation="MKVSDRRKFEKANFDEFESALNNKNDLVHCPSITLFESIPTEVR
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SVIWMNETLYETRIVPAIINVREWLDHMEANDPSPSVTNPYETSGYYAFSTVVPVLMG
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PTYYIPKVQFLTEAFDSEHTLATIGYKPNNKESYEITGFTSMGNGYGIKLFNYSVIHM
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complement(4753..5076)
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2393, 3004
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ISAEHGIGGHKKGKLHYTRSDIEIRFWKDIKNHYDPNGILNPKXI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17682 CCATTCACTATTATGTCATGTGACAACATGCCCCAAAATGGTGTCACAGTAAAGACCATG 17741
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/note="similar to D-lactate dehydrogenase from cerevisiae, Swissprot Accession Number P32891" /codon_start=1 /evidence=not_experimental /product="Yel071wp"
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                                                                                                                                                                                                                                                                                                                                                                                        Score 111.4; DB 8;
Pred. No. 8.8e-23;
0; Mismatches 316;
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3 \ \ 0	/gunction_regulator; Degradation of small molecules: /gunction_compounds" /action_compounds	/translation-"MKTLLIDANLGOARAYMAKTLLGAAARKAKLEIIDNPNDAEMA IVLGDSIPNDSADIOKNVWLGDISRAVAHPELELSEAKGHAKRYTAPVAATAPVAASG EKRVVAVTACPTOVAHTHRAAEAIETEAKKRGWWYKYETRGSVGAGNAITPEEVAAAD LVIVAADIEVDLAKFAGKPWYRTSTGLALKKTAQELDKAVAEATPYEPAGKAQTATSE GKNESAGAYRHLLTGVSYMLPWVAGGLCIALSFAGCITAFKEGTLAAALMOIGGGS AFALMYPVLAGYIAFSIADPPGLTPGLIGGMAVSTGSGFIGFIIAGFLAGYIAKIIS TOLKLPQSWEALKFTIIFLISLSSLVVGLAMIYLIGKPYAGILEGLITAFLAGYIAKIIS ILGAILGGMMCTDMGGPVNKAAYAFGSUGLLSTYGPMAAIMAAGMYPPLAMGLATMY	ARKKFDKAQDEGKAALVIGICFISEGAIPPAARDPMRVLPCIVGGAITGAISMAIG ARLMAPHGGLFVLIPGAITPVLGYLVAIIAGTLVAGLAYAFLKRPEVDAVAKAA" COMplement (4077 . :5015) /gene="fruk"	/note="73426" complement(40775015) /gene="futuk" /function="enzyme; Energy metabolism, carbon: Glycolysis" /note="Residues 1 to 312 of 312 are 100.00 pct identical to residues 1 to 312 of 312 from Escherichia coli K-12	/codon.start=1 /transl_table=11 /product="fructose-1-phosphate kinase" /profein id=%anG73n6 1"	/ DD_XTREFFILES AND 7.00.1. / AD_XTREFFILES AND 7.00.1. / AD_XTREFFILES AND 7.00.1. / AD_XTREFFILES AND 7.00.1. / AD_XTREFFILES AND 7.00.1. VARVIKULGIDVTWGGFLGRDNODGFOOLESELGIARFOVNGRTRINVKLFENDGE VTDFNFSGFEVTYPADWERFVTDSLSWLGGFDWVCSGLFSCVSPEAFTDWMTRLRSQ CPCITEDSSFRALVAGLKAAPWLVRPNRRELEIWAGRLPEWKDVIEAHALREGGIA HVVISLGAEGALWNNASGEMIAKPPSVDVVSTVGAGSSWVGGLIYGLLMRESSEHTLR LATAVAALAVSQSNVGITDRPQLAAMMARVDLQPFN"		/runction="enzyme; Transport of Smail molecules: Carbohydrates, organic acids, alcohols." //note="Residues I to 376 of 376 are 99.73 pct identical to residues I to 376 of 376 from Escherichia coli K-12 Strain MO1655: B2169"	/ COGUCL_Stathe=11 / Lransl_table=11 / product_"PTS system, fructose-specific IIA/fpr component" / protein_id="AAG57307.1" / db_xrefe="G1:12516495" / translation="MFQLSVQDIHPGEKAGDKEEAIRQVAAALVQAGNVAEGYVNGML AREQQTSFPGNGTAIPHQTTDTRODVLKTGVQVFOFPEGVTWGDGQVAYVAIGIAAS SDEHLGLLRQLTHVLSDDSVAEQLKSATTABELRALLMGEKQSEQLKLDNEMLTLDIV	
gene			gene	CDS			gene			gene
	: :									
S . Escherichia coli 0157:H7 EDL933. ISM Escherichia coli 0157:H7 EDL933 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			Direct Su L Submitted Wisconsin	source 11048— /organism=Escherichia coli 0157:H7 EDL933" /strain="EDL933" /serotype="0157:H7" /db_xref="taxon:155864" /note="enterchemorrhagic" /one complement/78 1015,	3	/function="orf; Unknown fundtion" /note="Residues 1 to 312 of 312 are 99.35 pct identical to residues 1 to 312 of 312 from Escherichia coli K-12 Strain MG1655: B2165" /codon_start=1	/protein_lo="Ad59/303.1" /db_xref="G1:125!491" /db_xref="G1:125!491" /translation="MSEKISPELLGISPEVODALKNKKPVVALESTIISHGMPFPQN AQTAIEVEETIRKQGAVPATIAIIGGVMKVGLSKEEIELLGREGHNVTKVSRRDLPFV VAAGKRGATWASTWIIAALAGIKVPRFTGGIGGVHRGAEHTFDISADLQELANTHVTV	VCAGABLILOLLITECTOFILICATIFICATISPEDSELARA MAAVKWOSGLNGGLVTANDEPEDFAMPEHTINAVIDQAVAEAEAGGVIGKESTPELLAR VAELTGGDSLKSNIQLVFNNAILASELAKEYQRLAG" complement(10041945) /gene="yell" /gene="yell"		/traisl_table=11 /product=putative kinase" /product=putative kinase" /protein_id="Ad657304.1" /db_xref="6"(1:12516492" /traislation="MREKDYV"IGSANIDAGYSHESLNYADSNPGKIKFTPGGVGR NIAQNIALLGNRAWLLSAVGSDFYGGSLLTGNNOSGVYVVCKLIVPGENTSSYLSLLD NTGENLVAINDMISNATTAFYLAOHREFIORAKVIVADCNISEEALANILDNAANVP VFVDPVSAWKCVKVRERLSQTITLRFPREIEAFTLSGTALSGREDVAKVAMFHQHGLN RLVLSMGGDGYYYSDLSGESGNRAPIKTNVINTGAGDAMMAGLASCWVDGMPFAESV RFAQGCSSMALSCEYTNNPDLSIANVISLYENDECLN
KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS AUTHORS TITLE JOURNAL MEDLINE	PUBMED REFERENCE AUTHORS	TITLE JOURNAL FEATURES	Ö Ö	CDS			əuəb	CDS .	

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1 (sites)
Makino, K., Yokoyama, K., Kubota, Y., Yutsudo, C.H., Kimura, S.,
Kurokawa, K., Ishli, K., Hattori, M., Tatsuno, I., Abe, H., Iida, T.,
Yamamoto, K., Ohnishi, M., Hayashi, T., Yasunaga, T., Honda, T.,
Sasakawa, C. and Shinagawa, H.
Complete nucleotide sequence of the prophage VT2-Sakai carrying the
complete nucleotide sequence of the prophage VT2-Sakai carrying the
derived from the Sakai outbreak
Genet. Syst. 74 (5), 227-239 (1999)
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Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (strain:0157:H7, sub_strain:RIMD 0509952)
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Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma subdivision; Enterobacteriaceae;
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Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                       9879 ACATTAATGCTGGATGAGCAAGCGCCGACACTGCGGATTAAAGATGTCGATTTAACACAA 9938
                          9819 TCAGGATTCGCCCATATCAGTGATTGCATGCAGGATCGCGCATTTCGCCATGCCGCCAGA 9878
                                                                                                                    CGCTACGTGACGGAAGATGTCATTCCTTGGCCGATAACGGTATCGATTTGCCAACC 1461
                                                                                                                                                                                                              Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Harata,T., Yokoyama,K., Murata,T., Tanaka,M., Tobe,T., Idda,T., Takami,H., Honda,T., Sasakawa,C., Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Comparative analysis of the whole set of rRNA operons between enterohemorrhagic Escherichia coli 0157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655
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H7 DNA, complete genome, section 11/20
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0157:H7 and genomic comparison with a laboratory strain K-12
DNA Res. 8 (1), 11-22 (2001)
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                                                                                                                                                                                                                                                                                                                                      9999 ATCGCGATGGATGCCACCAGAAATTACCG 10028
                                                                                                                                                                                                                                                                                                        1522 GTCGCTGCGGATGGTTTCTCGAAAATTCCG 1551
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Escherichia.
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Direct Submission
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Ohnishi,M.,
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Strain
                                                                                                             /product="putative transport"
/protein_id="AAG57308.1"
/db_xref="01:12516496"
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RNYFVLLFVGVFLSSFGSTANPQMFALAREHADKTGREAVMFSSFLRAQVSLAWVIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MOGVLACLPSGIPGIGLEIEGAVQHAPQPGRHSIRCSLKVNHRI
DEBAQYHLECTSKGANTTCPKGSSRVLCRDIFDIYNESAPRANIIKKGWYLNYNG
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YVDGNEYVFMGKEDYTPYTFTKDOIEEELLEMPEGGAMDMOVLTWGGLLALELPQTY
DLEIVETAPGIKGASASARNKPATLSTGLVIQVPEYLSPGEKIRIHIEERRYMGRAD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              re enzyme; Not classified"
to 488 of 488 are 98.36 pct identical to
of 488 from Escherichia coli K-12 Strain
of 393 are 99.23 pct identical to from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                        PLAYALAMGESFTVMYLSAAVAFIVCCVMVWLFLPSMQKELPLATGTVEAPRRNRRDT
LLLFVICTLMWGSNSLYIINMPLFIINELHLPEKLAGVMMGTAAGLEIPTWLIAGYFA
                                                                                                                                                                                                                                                                                                        KRLGKRFLMRVAAVGGVCFYAGMLMAHSPVILLGLQLLNAIFIGILGGIGMLYFQDLM
PGQAGSATTLYTNTSRVGWIIAGSVAGIVAEIWNYHAVFWFAMVMIIATLFCLLRIKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="putative factor; Not classified"
/note="Residues 1 to 275 of 275 are 99.63 pct identical
residues 1 to 275 of 275 from Escherichia coli K-12 Stra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1042 GATGTCATCGACTGGCTGAGTACAATACCACTTGCCCGAATACCATGGTTGACCGCATT 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1102 ACGCCTCGTCCGGCAGCAGCATCCCGGCACGGATCAAGGCTCAAACGGGTATTGCCGAT 1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9519 GAACTCGCCGGGTGGATAAAAGAACACGTCAGTTTTCCGGGAACCATGGTCGACCGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1162 AAAGCGCCGGTAATGGGCCGAAACCTTTATCCAGTGGGTCGTGGAAGATAATTTCCGTGAT
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/protein_id="AAG57310.1"
/db_xref="G1:12516498"
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Pred. No. 5.6e-22;
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393
to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Residues 1
residues 1 to 488
MG1655: B2172"
/note="Residues 1
residues 1 to 393
MG1655: B2170"
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/note="23430"
7845. .8672
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/gene="yeip"
/function="pu
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Matches 259;
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GFSLVAEGFGFVIPKGYLYAAIGFSVMIEALNOLAIFNRRRFLSANQTLRQRTTEAVM
RLLSGQKEDAELDAETASMLVDHGNQQIFNPQERRMIERVLNLNQRTVSSIMTSRHDI
EHIDLNAPEDEIRQLLERNUHTRLVYDGDDAEDLLGVVHVIDLLQQSLRGEPLNLRV
LIRQPLVFFETLPLLPALEQFRNARTHFAFVVDEFGSVEGIVTLSDVTETIAGNLPNE
VEEIDARHDIQKNAGGSWTANGHMPLEDLVQVYDFLDLDEKREYHTIAGLLMEYLQRIP
KPGEEVQVGDYLLKTLQVESHRVQKVQIIPLRKDGEMEYEV"
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TEKPEWQLRLQFPQLNLDNLIPLNETANGENGAAQQGQSQSTLPRPVISSRIDEPAYO
GLQGFTADILLQASNNYWRGNNFTDVATQWTNKSGLLEITQLQGKLNGGQVSLCTLD
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QAHVENADTRRECHNPQQNIQQAVERNGGDVKAAENPDNVTRLDRFTTDLTLKGGVYT
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FSLDSVITAVGWVDHLLVWMAAVVIAISLMLMASKPLTQFVNSHPTIVILCLSFLLMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MRKKLAFLDTSLDDLRAFPESSRQEIGYQLDRIQQGLNPYDWKP
FSTIGPGVREIRTRDADGIYRVMYVAKFEEAVYVLHCFQKKTQTTSQSDIDLAKRRYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YQLQLDGPLRWHVWPQLSILSGRMSLTAQGASQPLVRADNMRLDVALLPLLSHQLSVK
QVMLKGAVIQLTPQTEAVRSEDAPVAPRDNTLPDLSDDRGWSFDISSLKVADSVLVFQ
HEDDEQVTIRNIRLQMEQDPQHRGSFEFSGRVNRDQRDLTISLNGTVDASDYPHDLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKIETFDSVWDAVSDTPEQAENMRIRAELVTIINNWIEQQGFSQ
AQAASALGVTQPRISELARGKIQIFSIDKLITMMAHAGLHIQRIEVQYPHAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MRRFLTTLMILLVVLVAGLSALVLLVNPNDFRDYMVKQVAARSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ECs2869"
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/gene="ECs2869"
/note="unknown,similar to hypothetical proteins e.g.
gi|9106618|gb|AAF64382.1|AE003986_12 [xylella fastidiosa]
percent identity 60 in 105 aa"
                                                                                              /note="similar to YEGH_ECOLI gi|1788377 percent identity
99 in 549 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"unknown, similar to hypothetical protein (Xylella
fastidiosa] gb|AAF84486.1|AE003993_5 percent identity 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to ASMA_ECOLI gi|1788378 percent identity 99 in 617 aa (Conserved in E.coli K-12)" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="suppressor of ompF assembly mutants"
/protein_id="BaB36294.1"
/db_xref="GI:13362340"
                                                                                                                                                                                                                                                                                                /product="putative transport protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"hypothetical protein"
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/db_xref="G1:13362339"
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/transl_table=11
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/evidence=not_experimental
/transl_table=11
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/transl_table=11
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/gene="ECs2871"
complement(6814. .8667)
/gene="ECs2871"
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/gene="ECs2870"
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/gene="ECs2870"
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/protein_id="BAB36289.1"
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LFGHWDNECEIPDPYRKSRETFAAVYTLLERSARQWAQALNAEQV"
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mall:ken@gen.info.osaka-u.ac.jp, Tel:81-6-6879-8365, Fax:81-6-6879-2047)
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REBERSIGALMQNGDLNQNRLLYPGDLLYVPRNDLKVFVWGEVKKQSTLKMDFSGM
TLTBALGNARGIDWITSNASGIFVIRPLKGEGGRNGKIANIYQLDMSDATSLVMATEF
RLQPYDVVYVTTAPVSRWNRLINQLLPTIŞGVRYMTDTASDIINW
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DLDKMVNYPLTPRLIDQLRPRPNVARPNMTLESEIANYQYRVGPGDVLNVTVMDHPE
LTTPAGQYRSSSDTGNWVQPDGTMFYPYIGKVHVVGKTLAEIRSDITGRLATYIADPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to B2060_ECOLI gi|1788374 percent identity 99 in 732 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to WZA_ECOLI gi|1788376 percent identity 100 in 379 aa (Conserved in E.coli K-12)" /codon_start=1
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100 in 147 aa (Conserved in E.coli K-12)"
/codon_start=1
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/protein_id="BAB36290.1"
                                                                                                                                                                                                                                                                                                                                 O157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
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                                                                                                                                                                                                                                               Location/Qualifiers
1. .268857
/organism="Escherichia coli/strain="0157:H7"
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/transl_table-11
                                                                                                                                                                                                                                                                                                                                                                                                           /sub_strain="RIMD 0509952"
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/gene="ECs2866"
complement(2238. .2681)
/gene="ECs2866"
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complement
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GNWQQLNYSLQVDQLLRKHLQDEAKRRLNDWAERNKDSRNGKDVKKLLEKM"

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                                                                                                                                                                                                                                                    Db 193126 CCCTGCGCGATTAGCTGCGAACCGTTATCCAGTGGGTGGTGGAAGATAACTTCGTCGCT 193185
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                                                                                                                                                                                                                                                                                                                          1162 AAAGCGCCGGTAATGGGCGAAACCTTTATCCAGTGGGTCGTGGAAGATAATTTCCGTGAT 1221
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                                                                                                          Qy 1042 GAIGTCATCGACTGGCTGAGTACAAATACCACTTGCCCGAATACCATGGTTGACCGCATT 1101
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Score 108.4; DB 1; Length
Pred. No. 1.1e-21;
0; Mismatches 251; Indels
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Query Match 5.9%;
Best Local Similarity 50.8%;
Matches 259; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Positive selection system; metabolise; arabitol; ribitol; mannitol; transgenic cell; marker gene; arabitol dehydrogenase; ds.
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ABL29054
ABL19102
                                     AAH48024
AAS92760
AAL01054
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ABN16299
                                                                                                                                                                                                        AAS56324
AAZ99500
AAZ99506
                                                                                                                             AAS51468
ABLS6160
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 08-MAR-2001; 2001WO-US07474.
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15-AUG-2000; 2000US-025595.
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         GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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arabitol, ribitol which confer selective advantage on transformed FF X 8 X 000 000 000 000 X 8

Claim 1; Page 34-35; 37pp; English.

used in positively selecting transgenic cells from a population of cells unique the positive selection method, the presence of the gene of interest in the genetically transformed cells may be determined without the disadvantages associated with traditional negative selection systems. Positive selection of the transformed cells is achieved without transformed cells may be identified by simple visual means without transformed cells may be identified by simple visual means without the use of a separate assay to determine the presence of a marker gene. This technique also avoids the release of antibiotics or other dangerous genes into the environment. The present sequence is Escherichia coli The present invention relates to a positive selection system that involves conferring to transferred cells the ability to metabolise arabitol, ribitol and/or mannitol. The positive selection method is strain C arabitol dehydrogenase gene.

Sequence 1848 BP; 494 A; 443 C; 473 G; 438 T; 0 other;

ö 180 360 360 420 420 480 540 720 61 GCGTGGTATCTACACCGTTTGCAGGTGATGGCCGATAAACGCTGGAGACATTGCTGCGGGC 120 300 480 540 009 900 99 099 GTGCTGGAAACCGTCAGCCCGGAAGGGGTAAGCGAATATGAAGAGATCACCTCAATTCAG 240 241 AAGTTGATACCGTGGCAGGCAGATTTACAACCGCTGATTGCTGAAGGGGCCAGATCCGAAG 300 661 GTGCTGGAAACCGTCAGCCCGGAAGGGGTAAGCGAATATGAAGAGATCACCTCAATTCAG 720 Gaps 9 9 1 ATGAACGAACAATTTACATGGCTGCACATCGGGTTAGGTTCTTTTCATCGCGCACATCAG ACAAAAGTGATTGCTTTCACCGTCACCGAAGGCGGGTACTACCTGAATACCAGTCACAAA GCGTGGTATCTACACCGTTTGCAGGTGATGGGCGATAAACGCTGGAGCATTGCTGCGGGC 121 AATATTCGTAATGATGCTGAACATGTCGTACAGGCACTCAGTGCACAGAAGGTCGCTAT CTGGAAGTTAACAATCCTGATTTAGCGCCAGATCTTAAAGGGGGATGCAAAACAATTTAC GGTGTTATTACCCGTATCCTCGAAGCGCGTATGGCAAATAACGCCGGACCACTAACCCTG 481 ATGAACGAACAATTTACATGGCTGCACATCGGGTTAGGTTCTTTTCATCGCGCACATCAG GCGTGGTATCTACACCGTTTTGCAGGTGATGGGCGATAAACGCTGGAGCATTGCTGCGGGC 601 AATATTCGTAATGATGCTGAACATGTCGTACAGGCACTCAGTGCACAGAAAGGTCGCTAT DB 22; Length 1848; ö 0; Indels Query Match 100.0%; Score 1848; Best Local Similarity 100.0%; Pred. No. 0; Matches 1848; Conservative 0; Mismatches 541 61 181 181 301 361 481 421 q à g Q 엄 ò g ð qq ò a QQ a a g ò ò ò ð õ ò ò

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21 AAGTTGATACCGTGGCAGGATTTACAACCGCTGATTGCTGAAGGGGCAGATCCGAAG	TTCACCGTCACCGP	ATTTAGGGGCAGATCTTAAAGGGGGATGCAA	IGTTATTACCCGTATCCTCGAAGCGCGTATGGCAAATAACGCCGGACCACT	aattgcgataacgtgcgccataatggtgaacgtttccatgatggcctggttgagt	CCAGCTAACTGGCAAACAGGATGTCATCGACTGGCTGAGTACAATAC	IACCATGGTTGACCGCATTACGCCTCGGCGGCAGCAGCATCCGGCACGGATCAA	GGGTATTGCCGATAA	GAAGATAATTTCCGTGATGT	CCTATGAAGAGGGGAAGATTGGATTCTTAACTCTTCACACAGTTG	CGCCTGGGCAGGTACGTTAATCGGTCAAAATATATCCACGAAAGCACAATGACCGA	CTATCAGATTGCCGACCGCTACGTGACGGAAGATGTCATTCCTTGCTTG	GGTATCGATTTGCCAACCTACCGTGATGTTGTACTCAAGGGTTTTACCAAT	CAACGCGTCGCTGCGGATGGTTTCTCGAAAATTCCGGCGATGA	CGAGGCGTTCGCCCGAATGCCACCGCCATGTT	rgcactgttttacgtattcatggagcagtggcatcacggcaaactgcccta	GATGGCATCCTTGATGCACCAGCTGTCCATGCAATGTTACAGTCTGCCGATCCCGT	nagccagtgataaagcgctgtttggcgatttaaccga
72	78	8 84	9 9			106	114	120	126	132	138	144	150	156	162	168	174
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(SLDH) gene
                                                                                                                                                                                                                                                                                     Gluconobacter oxydans D-sorbitol dehydrogenase
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                                                                           AAA97430 standard; DNA; 4115
                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                 29-JAN-2001
AAA97430
ID
                                                                                                                                                NAMES OF THE STATE OF THE STATE
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D-sorbitol dehydrogenase; SLDH; L-sorbose production; NADP+ dependent; sorbitol; mannitol; arabitol; oxidation; 2-keto-L-gluconic acid; L-ascorbic acid biosynthesis; vitamin C; ds.

Gluconobacter oxydans

WO200055329-A1.

21-SEP-2000

2000WO-JP01608 16-MAR-2000;

99JP-0072810. 99JP-0224679. 17-MAR-1999; 06-AUG-1999; (FUJI) FUJISAWA PHARM CO LTD

Υ; Saito Noguchi Y, Matsuura M, Ichikawa C, Takata Y; Shibata T, Ic Yamashita M,

WPI; 2000-587530/55. P-PSDB; AAB23172.

Gluconobacter oxydans derived D-sorbitol dehydrogenase obtainable by culturing its gene-transformed host cells, useful for producing L-sorbose or 2-keto-L-gluconic acid as an intermediate in L-ascorbic acid production

9; Page 60-63; 72pp; Japanese. Claim

The invention relates to Gluconobacter oxydans D'sorbitol dehydrogenase (SLDH; AAB33172) and to the gene encoding it (AAA97430). SLDH has a molecular weight of about 54 kba and catalyses the conversion of D-sorbitol into L-sorbose using NADP+ as a co-enzyme. SLDH specifically catalyses the oxidation of sorbitol, mannitol and arabitol, but does not encompasses expression vectors and host cells comprising the close concompasses expression vectors and host cells comprising the Gluconobacter oxydans SLDH gene, and the recombinant production of SLDH. contacting the recombinant SLDH with D-sorbitol; a process for producing 2-keto-L-gluconic acid by contacting recombinantly produced sorbose dehydrogenase and/or sorbosone dehydrogenase with L-sorbose; and a process for preparing L-ascorbic acid or its alkaline earth metals salts by conversion from 2-keto-L-gluconic acid. SLDH is useful for producing L-sorbose or 2-keto-L-gluconic acid. SLDH is useful for producing L-sorbose or 2-keto-L-gluconic acid as an intermediate in L-ascorbic the Gluconobacter production. The present sequence represents SLDH gene.

Sequence 4115 BP; 833 A; 1133 C; 1270 G; 879 T; 0 other;

Query Match

TGCACATCGGGTTAGGTTCTTTTCATCGCGCACATCAGGCGTGGTATCTACACCGTTTGC 562 Similarity 46.8%; Score 105; DB 21; | Length 4115; Similarity 46.8%; Pred. No. 4.6e-24; | Onservative 0; Mismatches 560; Indels 18 Local Simi les 509; Best Loca Matches 503 ð

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1699 CCGTGCG 1705

1090 1150 1447 ATAACGTGCGCCATAATGGTGAACGTTTCCATGATGGCCTGGTTGAGTTTCTCCAGCTAA 1030 1219 TTGATCGCATCACCCCGACCGTTTCGGCGGAAATCGCCAAGAAGCTCAACGCGGCCAGTG 1278 GTATTGCCGATAAAGCGCCGGTAATGGGCGAAACCTTTATCCAGTGGGTCGTGGAAGATA 1210 1271 TCCCCTATGAAGAGGCGAAGATTCGCATTCTTAACTCTTCACACAGTTGCATCGCCTGGG 1330 1507 1638 1508 ACACCAACCAACGCGTCGCTGCGGATGGTTTCTCGAAAATTCCGGCGATGATTGCCCCCA 1567 .042 TCGAGGCCCTGCGTCGTCGTTGGGATGCCGGTGGTAAGGCATTTACGGTCATGTCCTGTG 1101 857 CTGATTTAGCGGCAGATCTTAAAGGGGGGATGCAAAACAATTTACGGTGTTATTACCCGTA 916 619 739 861 799 563 AGGTGATGGGCGATAAACGCTGGAGCATTGCTGCGGCAATATTCGTAATGA---TGCTG 619 CCGATCCGGAAGCCGTGCTGAAGCATCTTGTTGATCCGGCCATCCGCATCGTTTCCATGA 921 1459 CAGGCATTCTGGTCGGCTATGAGAATGTGGATGACGCCATTGAAGACAGCGAACTCCTTG 1579 TGACGCTCGAAGGCTATCGGGACAGCGTATCAGCCGTTTCTCCAACAAGGCGATGTCGG CCGTCACCGAAGGCGGGTACTACCTGA---ATACCAGTCACAAACTGGAAGTTAACAATC 917 TCCTCGAAGCGCGTATGGCAAATAACGCCGG-----ACCACTAACCCTGCTGAATTGCG CTGGCAAACAGGATGTCATCGACTGGCTGAGTACAAATACCACTTGCCCGAATACCATGG TTGACCGCATTACGCCTCGTCCGGCAGCAGAACTTCCGGCACGGATCAAGGCTCAAACGG 1211 ATTTCCGTGATGTCCGTCCGGCACTGGAGAGGTCGGTGTCGAACTGGTGGCGTCGTAA 1391 AGATTGCCGACCGCTACGTGACGGAAGATGTCATTCCTTGCTT---GGGCGATAACGGTA 1448 TCGATTTGCCAACCTACCGTGATGTTGTACTCAAGCGTTTTACCAATCCACATATTCAGG AACATGTCGTACAGGCACTCAGTGCACAGAAAGGTCGCTATGTGCTGGAAACCGTCAGCC CGTCCGGCAAGAGCACGGTGCGCGTCATGGGCGCGCTGCGTGACTATCTGCTTGCCCCGG CAGATTTACAACCGCTGATTGCTGAAGGGGCCAGATCCGAAGACAAAAGTGATTGCTTTCA TIGAACACGCTCCGGACTGGGCGATTGTTGGTGTTGGCCTGACGGGCAGTGACCGTTCAA CGGAAGGGGTAAGCGAATATGAAGAGATCACCTCAATTCAGAAGTTGATACCGTGGCAGG 1568 CACTGCG 1574 1102 1031 1159 1091 1331 682 680 802 740 862 800 971 1151 620 742 qq g ò QQ δ g ò Op ŏ g ŏ g ò a à qq ò g δ g ò ò qq õ g δý В ò g ò 음 ò q δλ

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1253 AACTGGTGGCGTCGGTAATCCCCTATGAAGAGGCGAAGATTCGCATTCTTAACTCTTCAC 1312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                          Set of genetically modified mutants not containing L sorbose reductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1193 AGTGGGTCGTGGAAGATAATTTCCGTGATGTCCGTCCGGCACTGGAGGTCGGTGTCG 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           953 TAACCCTGC#GAATTGCGATAACGTGCGCCATAATGGTGAACGTTTCCATGATGGCCTGG 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            607 CTGGGATACGC--GAAGGCCCGTGATCCGGAACTGGCCÁAGTGGATTGAAGAGAACGCGA 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a genetically engineered macroorganism derived from a malcoorganism belonging to the genus Gluconobacter or Acetobacter which is characterised in that the biological activity for reducing L-sorbose is substantially mullified by gene recombination. The present sequence encodes Gluconobacter suboxydans L-sorbose reductase.

N.B. This patent is equivalent to the basic NO9901197 in week 199949.
                                                                                                            Gluconobacter suboxydans; L-sorbose reductase; genetic engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                725 AGCTCAACGAAGCCAGTGGCCTGCACGACGACCTGCCGCTGCAGAAGACTTTCATC
                                                                                       Gluconobacter suboxydans L-sorbose reductase nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20; Length 1458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1458 BP; 329 A; 386 C; 434 G; 309 T; 0 other;
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/product= "L-sorbose reductase"
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                    AAZ35672 standard; DNA; 1458 BP.
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Best Local Similarity 51.4%;
Matches 310; Conservative
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AAZ32000 and AAZ32001 encode, and AAY49501 and AAY49502 represent, human metalloprotease thrombospondin (METH) proteins METH1 and METH2 respectively. METH1 and METH2 have been found to be potent inhibitors of anglogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to anglogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis,
                                                                                  1313 ACAGTTGCATCGCCTGGGCAGGTACGTTAATCGGTCAAAAATATATCCACGAAAGCACAA 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; angiogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; hammanioma; detection; arterial-venous malformation; immune deficiency; ss.
                                                                                                                                   965 CTGATCCCGATCTACGGGGTATCCTCGAGAACTTCCTGAACAAAAAGACGTCATCCCGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1025 TGAAGGCACCGCCGGGCATGACGCTGGAAGGCTATCGGGACAGCGTGATCAGCCGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                      1433 T---GGGCGATAACGGTATCGATTTGCCAACCTACCGTGATGTTGTACTCAAGCGTTTTA
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845 AGTTCGTTGGGGATGTGACGGACTACGAGCATGTAAAAATCCGCATGCTGAATGCTGGTC
                                                                                                                                                                                                                                          1373 TGACCGATTTTATCTATCAGATTGCCGACCGCTACGTGACGGAAGATGTCATTCCTTGCT
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                macula degeneration, haemangiomas, and arterial venous mainformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these cancer cancers or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory used for detection and diagnosis. AA322002 to AA322009, and AA445503 to AA445511 represent sequences given in the exemplification of the present
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endometrial bleeding disorders, diabetic retinopathy, some forms of
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Pred. No. 6.4e-18
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cancer therapy; benign tumour; coular anglogenic disease; rheunatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial anglogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb anglogenesis; obler Webber syndrome; wound granulation; plaque neovascularisation; telanglectasia; heemophilac joint; EST; anglofibroma; fibromuscular dysplasia; expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human METH1 and METH2, (ME for metalloprotease and TH for thrombospondin; see AAB50003 and AAB50003). The present sequence is an expressed sequence tag (EST) for METH. METH can be used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial anglogenesis,
7520 CCTACGAGGCGATGAAGATCCGCATCCTGAACGGGGGCCATGCGGTGATCGCCTATCCGT 7579
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disorders such as cancer,
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                                                                                                                                                                                                                                                                                                                                                                                            Crohn's disease; atherosclerosis; birth control; ss
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BETH ISRAEL DEACONESS MEDICAL CENT.
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99US-0144882.
99US-0147823.
99US-0373658.
99US-0171503.
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                                                                                                                                                                                             (first entry)
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Fornwald JA, Terrett JA;
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FORNWALD J
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JONAK Z L.
                                                                                                                                 AAC90082 standard;
                                                          7580 CGCCCTCATGG
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22-DEC-1999;
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AAS92759 standard; cDNA; 921

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coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler Webber syndrome, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also be used in pirth control. METH can also be used in diagnostic methods for the prognosis of cancer.
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                                                                                                                                                                                                                                                                                                                                            DB 22; Length 9810;
                                                                                                                                                                                                                                                                  Sequence 9810 BP; 1583 A; 3401 C; 3201 G; 1625 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches | 424; Indels
                                                                                                                                                                                                                                                                                                                                            1 4.7%; Score 87.6; DB 23 Similarity 48.1%; Pred. No. 6.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 410; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.4%; Score 80.6; DB 23; Length 921;
0.7%; Pred. No. 3.5e-16;
ve 0; Mismatches 189; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 921 BP; 230 A; 235 C; 230 G; 226 T; 0 other;
                                       encoding novel human diagnostic protein #28563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 28563; 103pp; English.
                                                                                                                                                                                                                                Tang YT;
                                                                                                                                                        30-MAR-2001; 2001WO-US08631
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23-AUG-2000; 2000US-0649167
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Matches 194; Conserv
                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                            P-PSDB; ABG28572
                                                                                                               WO200175067-A2.
                                                                                             Homo sapiens
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                      AGATTCGCATTCTTAACTCTTCACACAGTTGCATCGCCTGGGCAGGTACGTTAATCGGTC 1348
                                                                                                                                                             CTGCCTGGGAAGTCGCAGGTGTACAAATGGTGAATGATGTCCTGCCATGGGAAGAGATGA 798
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                                   ATAAGTTAATTGCACGTTTTGCTAATCCGGCGCTGAAACATAAGACCTGGCAAATCGCGA
                                                                                                              TGACGGAAGATGTCATTCCTTGGGCGATAACGGTATCGATTTGCCAACCTACCGTG
                                                                                                                                     TGCTGGATGAGCAAGCGCCGACACTGCAAATTAAAGATGTCGATTTAACACAATATGCGG
                                                                                         TCGCCCATATCAGTGATTGCATGCAGGATCGCCGATTTCGCCATGCCGCCAGAACATTAA
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                                                                                                                                                                                                                                                                                                                                                                                chromosome mapping; gene mapping; gene therapy; forensic; lpplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutation
responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                         novel human diagnostic protein #13860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 13860; 103pp; English.
                                                                                                                                                                                                         CGGATGGTTTCTCGAAAATTCCG 1551
                                                                                                                                                                                                                                                                                      BP
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                                                                                                                                                                                                                      Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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P-PSDB; ABG13869.
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The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human hote: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGCCGGTAATGGGCGAAACCTTTATCCAGTGGGTCGTGGAAGATAATTTCCGTGATGTC 1224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 CGTCCGGAATGGGAAAAAGCGGGAGCCGAACTGGTTAGCGATGTGCTGCTTATGAAGAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 ATGAAGTTGCGCATGCTCAACGGCAGTCATTCATTCCTGGCGTATCTTGCA 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGATATCAGCACATTAATGACTGTATGGAAGATGAACATTATCGTTATGCGGCGTATGGC
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                                                                                                                                                                                                                                                                                                                                                       23; Length 2810;
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                                                                                                                                                                                                                                                                                                                                                 Score 73.4; DB 23; Length
Pred. No. 1.9e-13;
0; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                              Sequence 2810 BP; 696 A; 699 C; 758 G; 657 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coding sequence fragment SEQ ID NO: 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGCGGATGGTTTCTCGAAAATTCCGGCGATGAT 1559
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                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                       4.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino
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                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 49.1
Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organic acid synthesis;
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AAF71527;
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                                                                                                                                                                                                          The present invention provides a number of 'nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly Liysine. The present sequence is a nucleic acid described note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                        mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                        Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1042 GATGTCATCGACTGGCTGAGTACAATACCACTTGCCCGAATACCATGGTTGACCGCATT 1101
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                                                                                                                                                                                8; SEQ ID NO: 126; 246pp + Sequence Listing; English.
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Pred. No. 4.7e-12;
"...matrhes; 257; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1509 BP; 341 A; 474 C; 376 G; 318 T; 0 other;
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 Ozaki A;
Ikeda M,
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Similarity 48.6%;
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Senoh A,
                                   WPI; 2001-376931/40.
                                                    P-PSDB; AAG89872.
Tatelshi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249;
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AAF71527 standard; DNA; 1632

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Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:335
                                                                                       SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitemin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
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                                                                            Corynebacterium glutamicum; carbon metabolism and energy production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids,
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99DE-1031428
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99DE-1042125
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                                                                                                                                                                                  Corynebacterium glutamicum.
                        (first entry)
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P-PSDB; AAB79410.
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                        30-APR-2001
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08-JUL-19
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           a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to (. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production
or nonproteinogenic amino acid (preferred), a purine or pyrimidine base,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     947 GGCCGCCCGCGTACGAGGTTGGCGTGCAGGTCGTCCGACGTGGAGGCTTATGAA 1006
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                                                                                                                                                                                                                                                                                                                                                                                                   770 GAGCTCGGCGAATGGGTGGAAAACAACGTGGCCTTCCCCAACTCCATGGTGGACCGCATC 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               830 ACCCCTGAAACCACCGACGCGACGCGATGACATCAAGG---AAATCGGCTACATCGAT 886
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                                                                                                                                                                                                                                                                                       Length 1632;
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                                                                                                                                                                                                                                                 Sequence 1632 BP; 374 A; 509 C; 400 G; 349 T; 0 other;
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                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                   Score 68.8; DB 22;
Pred. No. 5e-12;
0; Mismatches 257;
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                                                                                                                                                                                                                                                                                     3.7%;
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                                                                                                                                                                                                                                                                                       Query Match
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, Coryneform bacterium coryneform bacterium coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium, Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 121790 GAGCTCGGCGAATGGGTGGAAAACAACGTGGCCTTCCCCAACTCCATGGTGGACGCGTTC 121731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 121673 GCGTGGCCAGTGGTTTCTGAAGATTTCACCCAATGGGTCCTCGAGGATGCCTTCACCCAG 121614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DD 121730 ACCCCTGAAACCACGGACGGGAACGGGATGACATCAAGG---AAATCGGCTACATCGAT 121674
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                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1102 ACGCCTCGTCCGCCAGCAGCAGTTCCGGCACGGATCAAGGCTCAAACGGGTATTGCCGAT 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1042 GATGTCATCGACTGGCTGAGTACAATACCACTTGCCCGAATACCATGGTTGACCGCATT 1101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 121613 GGCCGCCCCCCCCGCTACGAGGTTGGCGTGCAGGTCGTCTCCCGACGTGGAGCCTTATGAA
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                                                                                                                                                                                                                                                   Yokoi
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Pred. No. 1.4e-10;
0; Mismatches 257; Indels 6;
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                                                                                                                                                                                                                                                   Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; SEQ ID NO: 1; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                   H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                                                                                                                   (KYOW ) KYOWA HAKKO KOGYO KK
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                                                                                                                    07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                               2000EP-0127688
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nes 249; Conservative
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                                                                                                                                                                                                                                                                                                                             WPI; 2001-376931/40
                                               18-DEC-2000;
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Tateishi N,
20-JUN-2001
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1314 CAGTTGCATCGCCTGGGCAGGTACGTTAATCGGTCAAAAATATATCCACGAAAGCACAAT 1373

319

379 AATGGTGAATGATGTCCTGCCATGGGAAGAGATGAAACTGCGGGATGCTTAATGGCAGCCA 320

GTGGGTGGTGGAAGATAACTTCGTCGCGGGGGTCCTGGGAAGTCGCAGGTGTACA 380

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               printed
from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity
                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #28872.
                                Db 121313 cecerereresegaarcereceacecarree 121282
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1519 CGCGTCGCTGCGGATGGTTTCTCGAAAATTCC 1550
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                                                                                                                           BP.
                                                                                                                        AAS93068 standard; cDNA; 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0540217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0649167
                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000;
23-AUG-2000;
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The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags \cdot
                                      1374 GACCGATTTTATCTATCAGATTGCCGACCGCTACGTGACGGAAGATGTCATTCCTTGCTT 1433
                                                                                                              1434 GGGCGATAACGGTATCGATTTGCCAACCTACCGTGATGTTGTACTCAAGCGTTTTACCAA 1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; se.
259 GGATCGCGCATTTCGCCATGCCGCCAGAACATTAATGCTGGATGAGCAAGCGCCGACACT 200
                                                                                                                                                     199 GCAAATTAAAGATGTCGATTTAACACAAATATGCGGATAAGTTAATTGCACGTTTTGCTAA 140
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                                                                                                                                                                                           1494 TCCACATATTCAGGACACCAACGACGCTGCGGGATGGTTTCTCGAAAATTCCG 1551
                                                                                                                                                                                                                 Clausen IG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus oryzae EST SEQ ID NO:5276.
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                                                                                                                                                                                                                                                                                                                                  BP
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0; Mismatches | 182;

Conservative

Local Similarity ses 176; Conserv

Query Match Best Loca Matches

3.6%; Score 66.8; DB 23; Length 1182; 49.2%; Pred. No. 1.9e'-11;

Qy 1194 GIGGETCGIGGAAGATATITCCGIGATGICCGICCGGCACIGGAGAAGGICGGIGICGA 1253

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Claim 1; SEQ ID No 18147; 103pp; English.
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discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering Using ESTS provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the analysis of the results. AAF0148 to AAF1147 represents ESTS from Aspergillus niger; AAF11854 to AAF11853 represents ESTS from Aspergillus niger; AAF11854 to AAF11854 to AAF1185 represents ESTS from Aspergillus oryzae; and
                                                                                                                                      AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                      TTGCCGATAAAGCGCCGGTAATGGGCCGAAACCTTTATCCAGTGGGTCGTGGAAGATAATT 1213
                                                                                                                                                                                                                                            1034 GCAAACAGGATGTCATCGACTGGCTGAGTACAAATACCACTTGCCCGAATACCATGGTTG 1093
                                                                                                                                                                                                                                                                                        1094 ACCGCATTACGCCTCGTCCGGCAGCAGAACTTCCGGCACGGATCAAGGCTCAAACGGGTA 1153
                                                                                                                                                                                                                                                                                                                                                   Gaps
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                               Score 61.2; DB 21; Length 684;
Pred. No. 1.1e-09;
                                                                                                                                                                                                                     0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                 TCCGTGATGTCCGTCCGGCACTGGAGGAGGTCGGTGTCGAACTGGT 1259
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 684 BP; 152 A; 212 C; 185 G; 135 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding novel human diagnostic protein #18147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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2000US-0649167.
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                                                                                                                                                                                                                     Matches 123; Conservative
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P-PSDB; ABG18156.
                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome
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23-AUG-2000;
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                     polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polymorleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1168 CCGGTAATGGGCGAAACCTTFATCCAGTGGGTCGTGGAAGATAATTTCCGTGATGTCCGT 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Internal standards useful for nucleic acid amplification assays, comprises a synthetic nucleic acid made by non-recombinant techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and to produce other types of data and products dependent on DNA and
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The invention relates to isolated polynucleotide (I) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rieger M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43.4; DB 2
Pred. No. 0.0025;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1228 CCGCCACTGGAGAAGGTCGGTGTCGAACTGGTG 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 859 CCTGCCTGGGAAGTCGCAGGTGTACAAATGGTG 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schwarz H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 22-27; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH48024 standard; DNA; 14041 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sest Local Similarity
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            The present invention relates to methods for the preparation and use of internal controls for nucleic acid amplification assays. The internal controls comprise a synthetic nucleic acid made by non-recombinant techniques. The internal controls are useful for detecting nucleic acids in a sample such as blood, spinal fluid, semen, saliva, tears, cell quantitative PCR assay, by adding the internal control to the sample, amplifying the nucleic acids in the sample and detecting the amplified products. The internal controls help in performing the nucleic acid amplification assay quickly, and inexpensitylely without sacrificing assay specificity or sensitivity. The present sequence is one such internal control, which was used in an example to likustrate the present
                                                                                                                                                                                                                                                            Note: the present sequence is the SEQ ID 8 shown in the sequence listing. This sequence differs from the SEQ ID 8 shown on page 13 of the disclosure (see AAH48038).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1285 GCGAAGATTCGCATTCTTAACTCTTCACACAGTTGCATCGCCTGGGCAGGTACGTTAATC 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2734 SSSCHGNCTDSWTHNANTRMYSHRTTMANDATVRYCNTCSTSASARSCADGNCTDSWTH 2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2794 SRSSCHASRAMGSYNTHSSRAWGBTCHAGBNBRGCRMANYTHANTCATNTHGNCTDSSYN 2853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1405 TACGTGACGGAAGATGTCATTCCTTGCTTGGCGGATAACGGTATCGATTTGCCAACCTAC 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1525 GCTGCGGATGGTTTCTCGAAAATTCCGGCGATGATTGCCCCCCACACTGCGAGGTGCTAC 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2971 MCNSMNGNSVRCATNANDTRACTNRCSSSNTHCASTHBGNCRARATNSTANDARDSNTHR 3030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1585 CAGCGAGGCGTTCGCCCGAATGCCACCGCCATGTTACCTGCACTGTTTACGTATTCATG 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                 2.3%; Score 42.4; DB 22; Length 14041; 18.8%; Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                            Sequence 14041 BP; 2151 A; 1354 C; 466 G; 2218 T; 7852 other;
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 18.8%; Pred. No. 0.017; ses 72; Conservative 132; Mismatches 177; Indels
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                                                                                                                                                                                                                                                  invention.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques of to restore normal activity of (II) or to treat disease states involving capters in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. (The polypeptide and polynuclectide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences AAS64197-AAS94564 represent novel human canno acid sequences and performed in electronic format directly from MIPO are the capter of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1256 TGGTGGCGTCGCTAATCCCCTATGAAGAGGCGAAGATTCGCATTCTTAACTCTTCACACA 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1316 GTTGCATCGCCTGGGCAGGTACGTTAATCGGTCAAAAATATATCCACGAAAGCACAATGA 1375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ATCGCGCATTTCGCCATGCCGCCAGAACATTAATGCTGGATGAGCAAAGCGCCGACACTGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 AAATTAAAGATGTCGATTTAACACAATATGCGGATAAGTTAATTGCACGTTTTGCTAATC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1496 CACATATTCAGGACACCAACCAACGGTCGCTGCGGATGGTTTCTCGAAAATTCCG 1551
                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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ilarity 45.6%; Pred. No. 0.13;
Conservative 0; Mismatches 161;
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                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 28564; 103pp; English.
                                                                                                                               Tang YT;
                  31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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Matches 135; Conservat
                                                                                                                                                                         WPI; 2001-639362/73
                                                                                                                               Drmanac RT, Liu C,
                                                                                   (HYSE-) HYSEQ INC.
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Search completed: March 21, 2003, 20:48:30 Job time: 805.996 secs

Title: Perfect score:

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Result

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Sequence 57, Appl
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Sequence 716, Appl
Sequence 35, App
Sequence 4, Appl
Sequence 4, Appl
Sequence 7, Appl
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Sequence 1, Appl
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                   Sequence 21,
Sequence 57,
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Sequence 10,
Sequence 2,
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
US-08-185-949B-75
US-08-070-301-21
US-08-070-301-21
US-08-105-764C-55
US-08-105-764C-55
US-08-1070-301-10
US-09-103-840A-1
US-09-103-840A-1
US-09-103-840A-1
US-09-102-248-4
US-09-102-248-4
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US-09-102-248-4
US-09-102-248-4
US-09-102-248-4
US-09-103-335-8
US-08-881-207A-74
US-08-881-207A-74
US-09-030-335-8
US-09-449-933-1
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APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: EALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08232463
Patent No. 5670367
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                 1400
1400
2095
3226
4403765
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11717
32768
1550
2625
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EDNESS: single
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US-08-232-463-14
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                              US-08-232-463-14/C
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STATE:
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Sequence 3, Appli
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8457.593 Million cell updates/sec
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                                                                                                                                                                                                                        1 atgaacgaacaatttacatg.......tctacgcgttaattaactaa 1848
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Sequence 47,
                                                                                                                    March 21, 2003, 09:44:37; Search time 67.0095 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                   GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-453-702B-264
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US-08-459-287-1
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US-08-674-169-47
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US-07-936-163-2
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US-09-709-126-3
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US-08-518-474-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                    - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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1848
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Match Length DB
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4797
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3220 GACCAAGCATCTTGGGGGGGGGGCGCGCTGAGTGGCAGGGGACAGGAGTACTTTGTTTCG 3279
   1074 TIGCCCGAATACCATGGTTGACCGCATTACGCCTCGTCCGGCAGCAGAACTTCCGGCACG 1133
                                                                            1134 GATCAAGGCTCAAACGGGTATTGCCGATAAAGCGCCGGTAATGGGCGAAACCTTTATCCA 1193
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                                       3160 TGGCTGGAAGATCCTGCGGGTGGGGCTTGGGGCTCACACACCTGTAGCACTTACTGGTAG
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62.2%; Pred. No. 1.4;
iive 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                               Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 264:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                         3280 TGGGGAGGTCTAATCTAGATATCGACTTGT 3309
                                                                                                                                                      1194 GTGGGTCGTGGAAGATATTTCCGTGATGT 1223
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US-09-453-702B-264/C
Sequence 264, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 264:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                  Burland,
Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1560 base pairs
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STRANDEDNESS: double
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Best Local Similarity 62.2%
Matches 51, Conservative
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                                                                                                                                                          83 AGGTGATGGGCGATAAACGCTGGAGCATTGCTGCGGGCAATATTCGTAATGATGCTGAAC 142
                                                                                                                                143 ATGTCGTACAGGCACTCAGTGCACAGAAAGGTCGCTATGTGCTGGAAACCGTCAGCCCGG 202
                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                         323 TCACCGAAGGCGGGTACTACCTGAATACCAGTCACAAACTGGAAGTTAACAATCCTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                    383 TAGCGGCAGATCTTAAAGGGGGATGCAAAACAATTTACGGTGTTATTACCCGTATCCTCG
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APPLICANT Bangur, Chaitanya S.
APPLICANT Bangur, Chaitanya S.
APPLICANT Fanger, Gary R.
APPLICANT L1, Samuel X.
APPLICANT L1, Samuel X.
APPLICANT Wang, Aijun
APPLICANT Henderson, Robert A.
APPLICANT Henderson, Robert A.
APPLICANT MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT APPLICATION NUMBER: US/09/643,597
SOFTWARE: FastSEQ for Windows Version 3.0
 Pred. No. 0.00029;
; Mismatches 199;
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51.3%; Pred. No. 1.5;
Live 0; Mismatches
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Patent No. 6426072
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)...(4797)
OTHER INFORMATION: n = A,T,C or G
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ilarity 10.2%; Pr
Conservative 198;
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Fan, Liqun
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ORGANISM: Homo sapien
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Best Local Similarity
Matches 45; Conserv
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2230 GATGCAGTATCTTCTGTTCGTGCAGATAGTTGACGCCATCGGCCACCTGACGAAAAATGT 2171
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TITLE OF INVENTION: No. 6365723el Sequences of E.
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Seay, Nicholas J.
REGISTATION UNDRER: 2736
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEFAHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32.4; DB Pred. No. 15; 0; Mismatches
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FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
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; MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-09-453-7028-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Blattner, Frederick
Burland, Valerie
                                                                                                                                                                                                                                               US-09-453-702B-62/c
; Sequence 62, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38129 CGGATCCATCGTCATTCCGTAA 38108
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US-08-459-287-1
S-quence 1, Application US/08459287
Patent No. 5686596
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Perna, Nicole T
Plunkett, Guy
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STRANDEDNESS: double
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Best Local Similarity 62.2%;
Matches 51; Conservative
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ZIP: 53701-2113
                                                               1071 CACTTGCCCG 1080
                                                                                                                           2170 AGCTTCCCAG 2161
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                                                                                                                                                                                                                           RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       956 CCCTGCTGAATTGCGATAACGTGCGCCATAATGGTGAACGTTTCCATGATGGCC 1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 51; | Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 1.7;
                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cahoon, Edgar B.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
TITLE OF INVENTION: ACTL-COA Oxidase Homologs FILE REFERENCE: BB-1175
CURRENT APPLICATION NUMBER: US/09/342,647A
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,482
EARLIER FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: MICROSOFT Office 97
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/770,170
CURRENT FILING DATE: 2001-01-26
CURRENT FILING DATE: 2001-01-26
CURRENT FILING DATE: 2001-01-26
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LIDIO NO 3
TYPE: N.
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                                                                                      Sequence 1, Application US/09342647A Patent No. 6368840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09770170 Patent No. 6319679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Michnoff, Carolyn
APPLICANT: Amezcua, Carlos
TITLE OF INVENTION: PAS Kinase
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Harper, Shannon
Rutter, Jared
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Best Local Similarity 55.3*
Matches 63; Conservative
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Matches 69; Conservative
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ORGANISM: Zea mays
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APPLICANT: McKnigh
                                                        JS-09-342-647-1/c
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1324 GCCTGGGCAGGTACGTTAATCGGTCAAAATATATCCACGAAAGCACAATGACCGATTTT 1383
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APPLICANT: Rubin, Gerald M.
APPLICANT: Pan, Duojia
APPLICANT: Rocke, Jenny
APPLICANT: Yavari, Reza
APPLICANT: Yavari, Reza
APPLICANT: Xu, Tian
TITLE OF INVENTION: KUZ: A No. 6190876el Family of Metalloproteases
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1444 GGTAFCGATTFGCCAACCFACGFGAFGTFGTACTCAAGCGFTTTFACCAAT 1494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 125; Indels
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,931
FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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268 BUSH STREET, SUITE 3200
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Pred. No.
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                                                                                                                                                                                                                                                         CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B97-0
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2796 base pairs
TYPE: NUCleic acid
STRANDENESS: Gouble
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US-09-285-502-3/c
; Sequence 3, Application US/09285502
; Patent No. 6190876
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Best Local Similarity 45.9%
Matches 106; Conservative
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STATE: CALIFORNIA
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; MOLECULE TYPE:
US-08-937-931-3
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Patent No. 5935792

GENERAL INFORMATION:
APPLICANT: Rubin, Gerald M.
APPLICANT: Rooke, Jenny
APPLICANT: Yavari, Reza
APPLICANT: Yavari, Reza
APPLICANT: Win Tian
TITLE OF INVENTION: KUZ: A No. 5935792e1 Family of Metalloproteases
NUMBER OF SEQUENCES: 10
CORRESPONDENCE: ADDRESS:
ADDRESSED NUMBER OF SEQUENCES: SEQUEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
         APPLICANT: Mukherjee, Ranjan
TITLE OF INVENTION: HUMAN PEROXISOME PROLIFERATOR ACTIVATED
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 3
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Pred. No. 1.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: IBM P.C. DOS (Version SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459, 287
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                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1286 CGAAGATTCGCATTCTTAACTCTTCACA 1313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/143,215
FILING DATE: October 25, 1993
APPLICATION NUMBER: 08/141,500
FILING DATE: October 22, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 204/138
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                    E: Lyon & Lyon
611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
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60.2%;
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TELEFAX: (213) 955-0440
TELERX: (7-3510
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1407 base pairs
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Matches 53; Conservative
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EDNESS: single
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CALIFORNIA
XY: USA
                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 536
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CITY: Los Angeles
STATE: California
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90017
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                                                                                                                                                                                                                                                                                                COUNTRY:
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STATE:
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Xu, Tian
TITLE OF INVENTION: KUZ: A NO. 6399350el Family of Metalloproteases
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                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 2796;
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/871,385A
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APPLICATION NUMBER: US/09/709,126
FILING DATE: 08-NO: 6599350-2000
APPLICATION NUMBER: 09/285,502
                 REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B97-081
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: OSMAN, RICHARD A REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 31-May-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-871-385A-3/c
; Sequence 3, Application US/09871385A
Pactent No. 6399350
; GENERAL INFORMATION:
                                                                                                                                                                                  LENGTH: 2796 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
RICHARD A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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Rooke, Jenny
Yavari, Reza
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                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.7%;
Best Local Similarity 45.9%;
Matches 106; Conservative
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COMPUTER READABLE FORM:
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TITLE OF INVENTION: KUZ: A No. 6319704el Family of Metalloproteases
NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.7%; Score 31; DB 4; Length 2796;
45.9%; Pred. No. 6.1;
tive 0; Mismatches 125;; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 08-No. 6319704-2000
CLASSIFICATION: <URKNOWN>
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                            08/937,931
                                                                                                         NAME: OSNAN, RICHARD A
REGISTATION NUMBER: 36,627
REFRENCE/DOCKET NUMBER: B97-C
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 343-434
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 3: SEQUENCE CHARACTERISTICS:
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Patent No. 6319704
GENERAL INFORMATION:
APPLICANT: Rubin, Gerald M.
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STATE: CALIFORNIA
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Rooke, Jenny
Yavari, Reza
                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   LENGTH: 2796 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 106; Conservative
                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                    FILING DATE:
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US-09-709-126-3/c
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    853 AGCTGAATTTGTACGTTTTTTCCTCAGAAGTTCTGGACCATTAGCAGCATGTTCTTCTTTG 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 793 AGGTATCTGTGTTACTTCCTCTACACCAGTCATCTGGTATTTCCTCATTCTTTCAAATAC 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 45.9%; Score 31; DB 4; Length 2796; Similarity 45.9%; Pred. No. 6.1; Osservative 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ELLIS, CATHERINE
APPLICANT: JACKSON, JEFFREY
APPLICANT: MAYER, RUTH
TITLE OF INVENTION: HUMAN DISINTEGRIN METALLOPROTEASE
TITLE OF INVENTION: RELATED TO DROSOPHILA KUZ GENE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSPE: RATHER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ FOR Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,234
FILING DATE: 25-AUG-1997
REFERENCE/DOCKET NUMBER: B97-081
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                   ; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-871-385A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: PRESTIA, PAUL F
RECISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70237
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2796 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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US-08-920-234-1/c
Sequence 1, Application US/08920234
; Patent No. 5922546
; GENERAL INFORMATION:
                                                          (415) 343-4342
                                                              TELEFAX: (415) 343-
INFORMATION FOR SEQ ID NO: 3:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   823 TCCGTAATATTTAAAGAACAAATGATCAGTCTGAATATAAAGCTGACAAGTATTTTTTC 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      763 AGCTGAAGTTGTACGTTTTTTCCTCAGAAGTTCTGGACCATTAGCAGCATGTTCTTGTTG 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  703 AGGTATCTGTGTTACTTCCTCTACACCAGTCATCTGGTATTTCCTCATTCTTTCAAATAC 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1444 GGTATCGATTTGCCAACCTACCGTGATGTTGTACTCAAGCGTTTTACCAAT 1494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643 TGAATGATCTGCACAGCCCCCTGAGGACCGTATTTATGGGGATAGTTAAT 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Thomas P. Condon
APPLICANT: Thomas P. Condon
APPLICANT: Shin Cheng Fluornoy
TITLE OF INVENTION: ANTISENSE MODULATION OF ADAM10 EXPRESSION
FILE REFERENCE: ISPH-0446
CURRENT APPLICATION NUMBER: US/09/527,154
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                           0; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 125;
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Best Local Similarity 45.9%; Pred. No. 6.9;
                                                                                                                                                                                                                                                              Score 31; DB 2
Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09527154 Patent No. 6228648 GENERAL INFORMATION:
                                                                                                                                                                                                                                                           Query Match 1.7%;
Best Local Similarity 45.9%;
Matches 106; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 3349 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 106; Conservative
                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (470)...(2716)
US-09-527-154-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: homo sapiens
                                                                                                                                                             MOLECULE TYPE: CDNA
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3054 Cornwallis Road
                                           STATE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    701 TGCACGTCTCGTTGCAACGCTAACGGATAATAACGCCGGATCAGCAACAGTAGCAACAGC 642
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Patent No. 6239264

GENERAL INFORMATION

APPLICANT: Poblimann, Rainer

APPLICANT: Steiner, Sabine

APPLICANT: Montry Christine

APPLICANT: Mendland, Jurgen

APPLICANT: Mendland, Jurgen

APPLICANT: Rechtle, Philipp

APPLICANT: Rechtle, Philipp

TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII

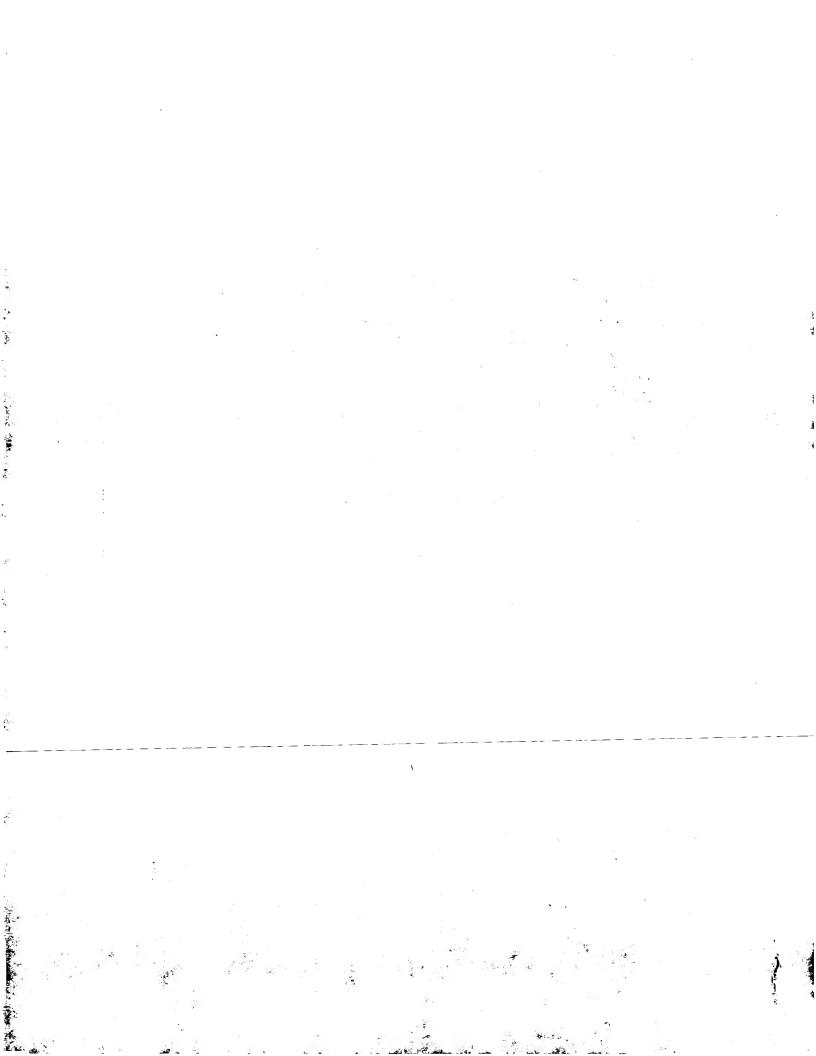
TITLE OF INVENTION: AND USES THEREOF

WUMBER OF SEQUENCES: 1152

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6239264artis Corporation
                                                                               APPLICANT: WALSH, TERENCE A
APPLICANT: WALSH, TERENCE A
APPLICANT: HOUTCHENS, ROBERT A
APPLICANT: STRICKLAND, JAMES A
APPLICANT: STRICKLAND, JAMES A
APPLICANT: ORR, GREGORY L
TITLE OF INVENTION: INSECTICIDAL PROTEINS AND METHOD FOR
TITLE OF INVENTION: PLANT PROTECTION
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSES: THOMAS D. ZINDRICK
STREET: 9002 PURDUE ROAD
CITY: INDIANAPOLIS
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1339;
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                                                                                                                                                                                                                                                                                                                                                                STALL:
COUNTRY: US
ZIP: 46268-1189
ZIP: 46268-1189
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBÜR: US/O7/936,163
FILLING BATE: 27-AUG-1992
FILLING PATE: 27-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCATCAACAAGATTGAACTCATATTTATCTCCATTAC 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.7%; Score 30.8; D
Best Local Similarity 57.1%; Pred. No. 4.4;
Matches 56; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 27-AUG-1992
CLASSIFICATION: 514
ATTCRNEY FAGENT INFORMATION:
NAME: ZINDRICK, THOMAS D
REGISTRATION NUMBER: 32,185
REFERENCE/DOCKET NUMBER: C-38,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-1869;
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1339 base pairs
TYPE: nucleic acid
STRANDENNESS: single
              Sequence 2, Application US/07936163
Patent No. 5743477
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-998-416-591/c
US-07-936-163-2/c
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945 CGGACCACTAACCCTGCTGAATTGCGATAACGTGCGCCATAATGGTGAACGTTTCCATGA 1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.7%; Score 30.6; DB 4; Length 699; Best Local Similarity 51.1%; Pred. No. 3.4; Matches 72; Conservative 0; Mismatches 69; Indels
                                                                           ZIP: 27/09
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFTCATION: 435
PRIOR APPLICATION NUMBER: CH 0016/97
APPLICATION NUMBER: CH 0016/97
APPLICATION NUMBER: CH 0016/97
APPLICATION NUMBER: 31-DEC-1996
ATTONEY/AGENT INFORMATION:
NAME: Meigs, J. Tinothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
RELEPHONE: 919-541-8587
TELEPHONE: 919-541-8587
INFORMATION FOR SEQ ID NO: 591:
CFOOTHER FOR SEQ ID NO: 591:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: March 21, 2003, 11:12:01 Job time : 166.009 secs
Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1065 AAATACCACTTGCCCGAATAC 1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 699 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (9e
CHGINAL SOURCE:
ORGANISM: PAG1406RP
US-08-998-416-591
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Sequence Sequence Sequence Sequence

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                                                        March 21, 2003, 11:05:17 ; search time 138.147 Seconds (without alignments) 10373.549 Million cell updates/sec
                                                                                                               1 atgaacgaacaatttacatg.......1ctacgcgttaattaactaa 1848
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Compugen Ltd
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                                                                                                                                                          538826 seqs, 387737923 residues
       GenCore version
Copyright (c) 1993 - 2003
                                          nucleic search, using sw model
                                                                                                                               IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                             seq length: 0 seq length: 2000000000
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Sequence:
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Maximum |
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Sequence 29, Appl Sequence 30, Appl Sequence 31, Appl Sequence 57, Appl Sequence 6, Appli Sequence 7, Appli Sequence 32, Appli Sequence 32, Appli Sequence 34, Appli Sequence 9, Appli Sequence 9, Appli Sequence 2430, Appli Sequence 2431, Appli Sequence 841, Appli Sequence 849, Appli Sequence 187, Appli Sequence 2460, Appli

US-09-843-250-1 US-09-843-250-25 US-09-843-250-29 US-09-843-250-29 US-09-843-250-30 US-09-843-250-30 US-09-843-250-56 US-09-843-250-57 US-09-843-250-6 US-09-843-250-6 US-09-843-250-6 US-09-843-250-7 US-09-843-250-7 US-09-843-250-3 US-09-843-250-3 US-09-843-250-3 US-09-843-250-3 US-09-764-869-2430 US-09-764-869-2430 US-09-764-869-2430 US-09-70-791-841 US-09-938-842-1409 US-09-938-842-1409 US-09-938-842-187-187-187-187-187-188-3

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9841 14462 3262 3262 341

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1800 2594 2796

ALIGNMENTS

RESULT 1 US-09-802-208B-1 US-09-802-208B-1 Sequence 1, Application US/09802208B Publication No. US20030041352A1 GENERAL INFORMATION: APPLICANT: LaFayette, Peter APPLICANT: LaFayette, Peter APPLICANT: Kane, Patrick TILLE OF INVENTION: Arabitol or Ribitol As Positive Selectable Markers FILE REPERENCE: UGA-855R CURRENT APPLICATION NUMBER: US/09/802,208B CURRENT FILING DATE: 2001-03-08 NUMBER OF SEQ ID NOS: 5 CORPUSED DATE: DATE OF TABLES OF	SEQ ID NO 1 : LENGTH: 1848 : TYPE: DNA : ORGANISM: Bscherichia coli US-09-802-208B-1	Query Match 100.0%; Score 1848; DB 9; Length 1848; Best Local Similarity 100.0%; Pred. No. 0; Matches 1848; Conservative 0; Mismatches 0; Indels 0; Gabs	GCTGCACATCGGGTTAGGTTCTTTTCATCGCGCACATCP	Qy 61 GCGTGGTATCTACACCGTTTGCAGGTGATGGCCGATAAACGCTGGAGCATTGCTGCGGGC 120 	QY 121 AATATTCGTAATGATGCTGAACATGTCGTACAGGCACTCAGTGCACAGAAAGGTCGCTAT 180	OY 181 GTGCTGGAAACCGTCAGCCCGGAAGGGGTAAGCGAATATGAAGATCACCTCAATTCAG 240	Qy 241 AAGTTGATACCGTGGCAGGCAGATTTACAACCGCTGATTGCTGAAGGGGCAGATCCGAAG 300
cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:* cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:* cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:* cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:* cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:* cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:* cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:* cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:* cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:* cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USOO_NEW_PUB.seq:* cgn2_6/ptodata/2/pubpna/USOO_NEW_PUB.seq:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	ult Query No. Score Match Length DB ID Description	1 1848 100.0 1848 9 US-09-802-208B-1 Sequence 1, Appli 2 68.8 3.7 1509 9 US-09-738-626-126 Sequence 126, App 3 15 1.9 653 9 US-10-184-644-402 Sequence 402, App 4 33.2 1.8 671 9 US-10-184-644-346 Sequence 346, App 5 33.2 1.8 671 9 US-10-184-644-346 Sequence 346, App	1.8 4797 10 US-09-480-716A-134 1.8 4797 10 US-09-880-107-3939 1.8 4797 10 US-09-880-107-3939 1.8 4797 10 US-09-880-107-3939 1.8 4797 10 US-08-987-778-134	32.8 1.8 615 10 32.8 1.8 919 9 32.4 1.8 1560 9 32.4 1.8 1560 9	9 US-10-114-170-62 10 US-09-815-242-9961 US-09-921-833-3	31.4 1.7 2176 9 U

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Published_Applications_NA:*

Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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q	241	AAGTTGATACCGTGGCAGGCAGATTTACAACCGCTGATTGCTGAAGGGGCCAGATCCGAAG 300	ċ	נסכר
à	301	CAAAAGTGATTGCTTTCACCGTCACCGAAGGCGGGTACTGCTGAATACCAGTCACAAA 3	Z 8	1381
g ,	301	m	Qy	1441
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ά	421	48	δy	1501
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λα	481	ATGAACGAACAATTACATGGCTGCACATCGGGTTAGGTTCTTTTCATCGCGCACATCAG 540	δλ	in i
q	481	ATGAACGAACAATTTACATGGTGCACATCGGGTTAGGTTCTTTTCATCGCGCACATCAG 540	q d	1561
γα	541	GCGTGGTATCTACACCGTTTGCAGGTGATGGCGCGATAAACGCTGGAGACATTGCTGCGGC 600	y g	1621
q	541	GCGTGGTATCTACACCGTTTGCAGGTGATGGCCGATAAACGCTGGAGCATTGCTGCGGGC 600	3 6	യ
oy Ob	601	AATATTCGTAATGATGCTGAACATGTCGTACAGGCACTCAGTGCACAGAAAGGTCGCTAT 660 	qa qa	9
ò	661	GTGCTTGGAAACCGTCAGGAGAGGGGTAAGGGGAATTATGAAGAGATCACCTCAATTCAG 720	δλ	1741
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á	721	AAGTIGAIACCGIGGCAGGCAGAITIACAACCGCIGAITGCIGAAGGGGCAGAICCGAAG 780	QY	œ
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දු ස	781	ACAAAAGTGATTGCTTTCACCGTCACCGAAGGCGGGTAC [†] ACCTGAATACCAGTCACAAA 840 		SULT 2 -09-738 Sequenc
ob Ob	841	CTGGAAGTTAACAATCCTGATTTAGCGGCAGATCTTAAAGGGGGATGCAAAACAATTTAC 900 		IDIICA ENERAL APPLICA
λ G	901	GGTGTTATTACCGGTATCCTCGAAGCGCGTATGGCAATAACGCCGGACCACTAACCCTG 960		APPLIC
λ a	961	10		APPLIC
. yo	1021	9 9		TITLE FILE R CURREN
λ O	1081	AATACCATGGTTGACCGCATTACGCCTCGTCCGGCAGAACTTCCGGCACGGATCAAG 1140 		RIOR PRIOR PRIOR
ž a	1141	GCTCAAACGGGTATTGCCGATAAAGCGCCGGTAATGGGCGGAACCTTTATCCAGTGGGTC 1200 		PRIOR PRIOR NUMBER SOFTWA
ž q	1201	GTGGAAGATAATTTCCGTGATGTCCGTCCGCACTGGAGAGGTCGGTGTCGAACTGGTG 1260 	v,	LENGT LENGT TYPE: ORGAN
λς q	1261	GCGTCGGTAATCCCCTATGAAGAGGCGAAGATTCGCATTCŤTAACTCTTCACAGAGTTGC 1320 	n-sn	Query M Best Lo
λχ op	1321	ATCGCCTGGGCAGGTACGTTAATCGGTCAAAATATATCCACGAAAGCACAATGACCGAT 1380 	MS Qy	1042
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AACGGTATCGATTGCCAACCTACCGTGATGTTGTACTCAAGCGTTTTACCAATCCACAT 1500
                                                                                                                                                                                                                                                                    GCTGTTTATGCCAGTGATAAAGCGCTGTTTGCCATTTAACCGAACGTGAAGATTTTGCC 1800
                                                                                                                                                                                   GCCCCCACACTGCGAGAGTGCTACCAGCGAGGCGTTCGCCCGAATGCCACCGCCATGTTA 1620
                                                                                                                                                                                                                                                                                                                                CCTGCACTGTTTTACGTATTCATGGAGCAGTGGCATCACGGCAAACTGCCCTATGAATAT 1680
                                                                                                                                                                                                                                                                                                                                                                                                            CAGGATGGCATCCTTGATGCACCAGCTGTCCATGCAATGTTACAGTCTGCCGATCCCGTC 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GATGTCATCGACTGGCTGAGTACAAATACCACTGCCCGAATACCATGGTTGACGCATT 1101
                                                                                                                                                                ATTCAGGACACCAACCAACGCGTCGCTGCGGATGGTTTCTCGAAAATTCCGGCGATGATT 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Gaps
                                                                                 AACGGTATCGATTTGCCAACCTACCGTGATGTTGTACTCAAGCGTTTTACCAATCCACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 3.7%; Score 68.8; DB 9; ocal Similarity 48.6%; Pred. No. 2.1e-12; s 249; Conservative 0; Mismatches 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEE OF INVENTION: NOVEL POLYNUCLEOTIDES

JE REFERENCE: 249-125

RRENT APPLICATION NUMBER: US/09/738,626

RRENT FILING DATE: 2000-12-18

COR APPLICATION NUMBER: JP 99/377484

COR APPLICATION NUMBER: JP 00/159162

COR APPLICATION NUMBER: JP 00/280988

COR APPLICATION NUMBER: JP 00/280988

COR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ce 126, Application US/09738626 ation No. US20020197605A1 INFORMATION:
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LICANT: MIZOGUCHI, HIROSHI
LICANT: ANDO, SEIKO
LICANT: ANDO, SEIKO
LICANT: OCHIAI, MKIRO
LICANT: YOKOI, HARUHIKO
LICANT: YOKOI, HARUHIKO
LICANT: TATEISHI, NAOKO
LICANT: SENOH, AKIHIRO
LICANT: IKEDA, MASATO
LICANT: OZAKI, AKIO
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Smith, Victoria
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                                                                                                                                         GTCCGTCCGGCACTGGAGAAGGTCGGTGTCGAACTGGTGGCGTCGGTAATCCCCTATGAA 1281
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                                                                                  1162 AAAGCGCCGGTAATGGGCGAAACCTTTATCCAGTGGGTCGTGGAAGATAATTTCCGTGAT 1221
                                                                                                               846
670 GAGCTCGGCGAATGGGTGGAAAACAACGTGGCCTTCCCCAACTCCATGGTGGACCGCATC 729
                                           TATTCGTAATGATGCTGAACATGTCGTACAGGCACTCAGTGCACAGAAGGTCGCTATGT 662
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                                                                                                ACGCCTCGTCCGGCAGCAGAACTTCCGGCACGGATCAAGGCTCAAACGGGTATTGCCGAT
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1 Similarity 7.1%; Pred. No. 0.15;
38; Conservative 159; Mismatches 336; Indels
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US-10-184-644-402
; Sequence 402, Application US/10184644
; Serview No. US20030044930A1
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Best Local Similarity 7.1%;
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Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang, Zemin
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                       783 AAAAGTGATTGCTTTCACCGTCACCGAAGGCGGGTACTACCTGAATACCAGTCACAAACT 842
                                                                                                                                                                                                                                                                               843 GGAAGTTAACAATCCTGATTTAGCGGCAGATCTTAAAGGGGGGATGCAAAACAATTTACGG 902
                                                                                                                                                                                                                                                                                                                       GITGATACCGTGGCAGGCAGATTTACAACCGCTGATTGCTGAAGGGGCAGATCCGAAGAC 782
                                                                   177 GDPLSYYQTGDIIRAGIKDIDRYHEKLAVSLYSSSLPPHLSGIKLGVISSEELPLYYRRS 236
                                                                                                                                                                                                    VELNSNSLESYENVMQSSLGFVNPGVVEFLLEKLGIDESNPPSLMRGLQSKNFSEDDFAS
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00; Mismatches 117; Indels
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CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
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(Sequence 346, Application US/10184644

) Sequence 346, Application US/10184644

) Publication No. US20030044930A1

) GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian
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Best Local Similarity 7.3%; Pre
Matches 17; Conservative 100;
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LENGTH: 4797
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...MTCHSHTMSHSHSTS.IMMMMYCC..CYY.IYBTIMM..A.H.HSAM.S.SSS.SN.
                                                                                                                                             1623 TGCACTGTTTTACGTATTCATGGAGCAGTGGCATCACGGCAAACTGCCCTATGA 1676
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APPLICANT: Bangur, Cary R.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Gary R.
APPLICANT: Anoger, Gary R.
APPLICANT: Samel X.
APPLICANT: Samel X.
APPLICANT: Mang, Aljun
APPLICANT: Moneill, Patricia D.
APPLICANT: Henderson, Robert A.
APPLICANT: Moneill, Patricia D.
APPLICANT: ANOGER, Neil
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: 2000-12-12
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
COFFURABRE F. FASTER OF THIS MALONS OF THE THANKEN AND THANKEN
                                                                                                                                                                                           Length 4797;
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Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455615
CURRENT APPLICANTION NUMBER: US/09/850,716A
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Pred. No. 5;
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Patent No. US20020052329A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-735-705-134
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Best Local Similarity 51.3
Matches 77; Conservative
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Fan, Liqun
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ORGANISM: Homo sapien
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US-09-850-716A-134
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APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
ITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT PILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SED ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
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51.3%; Pred. No. 5;
:ive 0; Mismatches
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0; Mismatches
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51.3%; Pred. No. 5;
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NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 134
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LOCATION: (1)..(4797)
OTHER INFORMATION: n = a or c or g or t
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                                                                                                                                                                                           ; LOCATION: (1)...(4797)
; OTHER INFORMATION: n = A,T,C or G
US-09-850-716A-134
                                                                                                                                                                                                                                                                                                                   51.3%;
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Best Local Similarity 51.3
Matches 77; Conservative
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Matches 77; Conservative
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                                                                                                                                                                       NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
                                                                                               TYPE: DNA
ORGANISM: Homo sapien
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US-09-880-107-3939
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Length 596;

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CCAGCGAGGCGTTCGCCCGAATGCCACGCCATGTTACCTGCACTGTTTTACGTATTCAT 1643
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                            Mismatches 221;
                                                                                                                                                                DB 9;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 06/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,578
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                             1.8%; Score 32.8;
17.1%; Pred. No. 1.
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                                                                                                                                                                                      Best Local Similarity 17.1%; Pro
Matches 68; Conservative 108;
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Xu, H. Howard
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Wall, Daniel
Trawick, John D.
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APPLICANT: Haselbeck, Robert
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 310
LENGTH: 596
TYPE: PRT
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                                                                                                 Sapien
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                                                                                            ORGANISM: Homo
                                                                                                      ; ORGANISM: HOMOUS-10-184-644-310
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APPLICANT: Marnerakis, Margarita
APPLICANT: Marnerakis, Margarita
APPLICANT: Panger, Gary R.
APPLICANT: Carter, Darrick
APPLICANT: Wedvick, Thomas S.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Penger, Neil
TILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: AAAAA
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51.3%; Pred. No. 5;
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; LOCATION: 135, 501, 4421, 4467, 4468, 4698
; OTHER INFORMATION: n = A,T,C or G
US-09-897-778-134
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  3280 TGGGGAGGTCTAATCTAGATATCGACTTGT 3309
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CURRENT APPLICATION NUMBER: 2002-06-28
CURRENT FILING DATE: 2002-06-28
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Publication No. US20030044930A1
                                                                                                               Sequence 134, Application US/09897778 Patent No. US20020147143A1
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Matches 77; Conservative
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APPLICANT:
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1164 AGCGCCGGTAATGGGCGAAACCTTTATCCAGTGGGTCGTGGAAGATAATTTCCGTGATGT 1223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plunkett,
Welch, Ro
                                                                                                                                                                                                                                                                                                                                      32 ..CNNN.M..SANS.D 17
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-114-170-264/c
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                                                                                                                                                                                                               1645 GAGCAGTGGCATCACGGCAAACTGCCCTATGAATATCAGGATGGCATCCTTGATGCACCA 1704
                                                                                                                                                                                                                                                                                      1705 GCTGTCCATGCAATGTTACAGTCTGCCGATCCCGTCGCTGTTTATGCCAGTGATAAAGCG 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     984 TAATGGTGAACGTTTCCATGATGGCCTGGTTGAGTTTCTCCAGCTAACTGGCAAACAGGA 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1044 TGTCATCGACTGGCTGAGTACAAATACCACTTGCCCGAATACCATGGTTGACCGCATTAC 1103
                                                                                                                                                                                                                                   POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           924 AGCGCGTATGGCAAATAACGCCGGACCACTAACCCTGCTGAATTGCGATAACGTGCGCCA 983
                                                                                                                                                                                                                                                                                                                            144 CGACGCCATGCACTGCAGGATGATGCCGATGCAGGCCATGGACATGGAGATGTTCAAGAA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                452 .MSK..BI.HTTYC.I..DB.TCS.MB.H.GSSTANH.CHA...B.SCH..SD..C.B..
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                                                                                                                                    Length 615;
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                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
                                                                                                                                      DB 10;
                                                                                                                                  Score 32.8; DB 10;
Pred. No. 1.8;
0; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Gord, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Abang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4050 LENGTH: 615
                                                                                                                                                                                                                                                                                                                                                                 1765 CTGTTTGGCGATTTAACCGAACGTGAAG 1792
                                                                                                                                                                                                                                                                                                                                                                                                     84 CTGCTGCATGCTGATGGCGAAGATGATG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 258, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                  Match 1.8%;
Local Similarity 51.4%;
Les 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-184-644-258/C
                                                                                            US-09-815-242-4050
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                                                                                                                                      Query Match
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TITLE OF INVENTION: No. US20030023075Alel Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
                                                      1224 CCGTCCGGCACTGGAGAAGGTCGGTGTCGAACTGGTGGCGTCGGTAATCCCCTATGAAGA 1283
                                                                                                                                                                  1284 GGCGAAGATTCGCATTCTTAACTCTTCACAGGTTGCATCGCCTGGGCAGGTACGTTAAT 1343
                                                                                                                                                                                                                                                                               212 .YGTYS.GSCC.GMRBYNYCS.CTSGYAT...MSMTYR...H.NR.H.BCWY.DTW.DB. 153
                                                                                                                                                                                                                                                                                                           92 YMR...N.MWN.....SBNM...YM.AT...RASTAABKH......M.H..BS.H.B.B.H.33
272 ASY. NGM.N., S.T., NDAM.NG., BBSH.S.K.R.STM.A.BMH., GHMCR.MAASH
                                                                                                                                                                                                                      152 .MC..CR.N.MMC...H.A.D.R.CM.CG.A..MAR..HYC..A..TB.BHTDMDN.DM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32.4; Di
Pred. No. 4.4;
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 264:
US-10-114-170-264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blattner, Frederick F
Burland, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 264, Application US/10114170 Publication No. US20030023075A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251-9166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perna, Nicole T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (608) 251-9: INFORMATION FOR SEQ ID NO: 264 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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APPLICANT:
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                                                                  553 CACCGTTTGCAGGTGATGGGCGATAAACGCTGGAGCATTGCTGCGGGCAATATTCGTAAT 612
  Gaps
                                            765 AGGGGCAGATCCGAAGACAAAGTGATTGCTTTCACCGTCACCGAAGGCGGGTACTACCT 824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: TIMMICK, JOHN D.
APPLICANT: Cart, Grant J.
APPLICANT: Cart, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR PELLY CATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SUPPLY FALLS DATE: 2001-02-16
SUPPLY FALLS DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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  31; Indels
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Pred. No. 5.9;
0; Mismatches 61;
  0; Mismatches
                                                                                                                                                                                                                                                                                              Sequence 7778, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                  825 GAATACCAGTCACAAACTGGAA 846
                                                                                                                                                                               165 CGGATCCATCGTCATTCCGTAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind, Judith W. Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%;
Best Local Similarity 53.1%;
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen, Kari L.
51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    673 GTCAGCCCGG 682
                                                                                                                                                                                                                                                                    US-09-815-242-7778/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1).
US-09-815-242-7778
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US-10-114-170-62/C
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LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 7778
LENGTH: 2436
Matches
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                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. US20030023075Alel Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 AGGGGCAGATCCGAAGACAAAAGTGATTGCTTTCACCGTCACCGAAGGCGGGTACTACCT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Indels
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REGISTRATION WUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01.Apr-2002
CLASSIFICATION: <un>
CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-10-114-170-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-815-242-9961
; Sequence 9961, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
. APPLICANT: Zyskind, Judith W.
                                                                    GENERAL INFORMATION:
APPLICANT: Blattner, Frederick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: (608) 251-5000
(608) 251-9166
Sequence 62, Application US/10114170 Publication No. US20030023075A1
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                                                                                                                                                                                                     Perna, Nicole T.
Plunkett, Guy
Welch, Rod
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STRANDEDNESS: double
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Best Local Similarity 62.25
Matches 51; Conservative
                                                                                                                                                                   Burland,
                                                                                                                                                                                                                                                                                   Welch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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Run on:

Sequence:

Searched:

Database

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AZ115205 RPCI-23-4
AL098149 DIOSOSPhil
BG268636 1000205G1
AW11987 618047B01
AW11987 618047B01
AW11087 618047B01
AV110366 Zea mays
AZ163357 SE_0073_B
AZ16357 SE_0073_B
BG724574 ELESTEG88
BM321997 ELESTEG20
BM321994 ELESTEG20
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BG561744 ELEGTGGGG
BG561164 ELESTGGGG
BG418689 HVSMEX002
BF420883 OV1_12_DO
BE848253 uu35h04.y
AZ568679 250PvG01
AZ568679 250PvG01
AZ568679 250PvG01
AL146023 Anopheles
AV634532 AV634532
BQ809588 1030012A1
AZ219883 Sheared D
BQ822949 103010580
AL240941 Tectraodon
AZ579022 30b10 Sho
BQ16397 B52082B12
BM660708 952041B05
AL628755 AL628755
AL106337 Drosophil
BM660708 952041B05
BM660708 952041B05
AL106337 Drosophil
BM660708 SEPCOM_SO
BM570033 EBFOOW_SO
BM570033 EBFOOW_SO
BM570033 EBFOOW_SO
BM570033 EBFOOW_SO
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AG-ND-144F15.TR ND-TAM Anopheles gambiae genomic clone AG-ND-144F15
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Anopheles.

(bases 1 to 801)

Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.

Direct Submission of BAC-end sequences from Anopheles gambiae

Other_GSSs: AG-ND-144F15.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (FIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208
Fax: 301 838 3543
Email: bloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                           BG561744
BG561164
BE028322
BG418689
BF420883
BE848653
AZ568609
AZ568679
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AV634532
BQ809588
AZ219883
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BQ163790
BM660708
AL628755
                         BG268636
AW15487
AW171987
AO500296
AY110366
AZ163357
ABA770826
BM371987
AI757652
BM321994
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AI068997
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AZ579022
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African malaria mosquito.
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BH395246
BH395246.1 GI:17341387
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AUTHORS
TITLE
JOURNAL
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AZ139030 SP_0178_B
BG608411 296895 MA
AL156645 Mopheles
AZ57838 28a07 Sho
AQ758091 HS_555_A
                                                                      (without alignments)
10552.182 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                    March 21, 2003, 15:18:35; Search time 2836.31 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                  32308132
                 Compugen Ltd.
       GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compug
                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                               16154066 seqs, 8097743376 residues
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Maximum Match 100%
Listing first 45 summaries
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AZ139030
BG608411
CNS01QW5
AZ578838
                                            nucleic search, using sw model
                                                                                                                                    IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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em_gss_other:*
em_gss_pro:*
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em_gss_fun:*
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88.2
81.6
62.4
39.2
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Perfect score:
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Maximum DB
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204 c
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VERSION
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BG608411
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                         TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                      ij
to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII Seq primer; MI3 Rev Class: BAC ends.
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Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota: Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea: Eucechinoidea: Echinodea: Echinoidea;
Strongylocentrotidae; Strongylocentrotus.

[ (bases 1 to 761)
Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
Swarzaell, S., Wallace, Lehrach, H., Britten, R.J, Davidson, E.H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1072 ACTTGCCCGAATACCATGGTTGACCGCATTACGCCTCGTCCGGCAGCAGAACTTCCGGCA 1131
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κ
                                                                                                                                                                                                                                                                                                                                                                         Score 90.8; DB 17; Length 801;
Pred. No. 1.4e-16;
0; Mismatches | 232; Indels 3
                                                                                                                                                                                                                           /db_xref="taxon:7165"
/clone="AG-ND-144F15"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
1 162 c 156 g 273 t
                                                                                                                                                                                      /organism="Anopheles gambiae"
/strain="PEST"
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Best Local Similarity 50.88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 AAAATCGAACAACTTACCGGTGTGCGCGATCCTGCGGGCGTTGCCTGTGAACCTTTCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 CATTCATTCCTGGCGTATCTGGGGTATCTTGCAGGATATCAGCACATTAATGACTGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1132 CGGATCAAGGCTCAAACGGGTATTGCCGGTAAAGCGCCGGTAATGGGCGGAAACCTTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 TIGAAAGIGCAGGGCGIIGAITIGCAAGAITACGCIAACCGAITAATIGCACGCIATAGC
A sea urchin genome project: Sequence scan, virtual map, additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000) 20402566
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BG608411
BG608411. GI:13658389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.8%; Score 88.2; DB 17;
ilarity 50.3%; Pred. No. 8.4e-16;
Conservative 0; Mismatches 213;
                                                                                                                         Contact: Cameron, RA, Davidson, EH, Hood, Division of Biology 156-29
California Institute of Technology Pasadena california 91125, USA
Fer: (626) 395-8421
Frax: (626) 793-3047
Email: acameron@caltech.edu
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Seq primer: T7
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Location/Qualifiers
1. .761
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Anophers:

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Genoscope.

Direct Submission

Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Chases 1 to 799)

SRoth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.

Direct Submission

L. Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.

Roux, Paris 75015, France

This clone is from an A. gambiae BAC library provided by F.H.

Collins and sequenced by Genoscope in collaboration with the Darkov of Biochem, and Biol. Molec. of Insects, Institut
                                              CNSULUWD TO THE TABLE TO THE TRANSPORT OF THE TRANSPORT TO THE TRANSPORT OF NOTICEDENCE TO THE TRANSPORT OF ALTERNATION PEST Of Anopheles gambiae (African malaria mosquito), 99116648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1111 CCGGCAGCAGAACTTCCGGCACGGATCAAGGCTCAAAACGGGTATTGCCGATAAAGCGCCG 1170
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                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Pred. No. 8.6e-08;
1; Mismatches 151; Indels
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    /organism="Anopheles gambiae"

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/clone="31M20"
/clone_lib="NotreDame1"
/note="end : SP6"
a 245 c 206 g 167
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                                                                                                                                                                                                                     African malaria mosquito.
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AL156645.1 GI:7017564
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Best Local Similarity 51.4%;
Matches 164; Conservative
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                          RESULT 4
CNS01QW5/c
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                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4396
Fax: 402 762 4390
Fax: 402 762 4390
Single pass sequencing. Bases called and alt_trimmed with phred
VO.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                        Casas, E.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 506)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                  Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Sall; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1112 CGGCAGCAGAACTTCCGGCACGGATCAAGGCTCAAACGGGTATTGCCGATAAAGCGCCGG 1171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACKWARD: GTTTTCCCAGTCACGACG
Plate: 1 row: A column: 22
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH108"
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                                                                                                                                                                      EST discovery in swine Unpublished (2000) Contact: Smith TPL
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 28a07 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium sp. NGR234 genomic clone 28a07, DNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 391)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Shot-gun genomic library of Rhizobium strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: M13; derivative strain of NGR234 cured of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1045 GTCATCGACTGGCTGAGTACAAATACCACTTGCCCGAATACCATGGTTGACCGCATTACG 1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HS_5552_A1_A07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1128 Col=13 Row-A, DNA sequence.
AQ758091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                           Contact: Virginie Viprey
Laboratoire de Biologie Moleculaire des Plantes Superieures
University of Geneva
1. Chemin de 1/Imperatrice, Chambesy/Geneva 1292, Switzerland
Tel: +44(0)1603450000
                                                                                     Rhizobium sp. NGR234.
Rhizobium sp. NGR234
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                        1 (bases 1 to 244)
Viprey,V., Rosenthal,A., Broughton,W.J. and Perret,X.
Genetic snapshots of the Rhizobium species NGR234 genome
Genome Blol. 1 (6), RESEARCH0014 (2000)
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Pred. No. 0.69;|
0; Mismatches 199; Indels 0
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                                                                                                                                                                                                                                                                                                                               Fax: +44(0)1603450045
Email: virginie.viprey@bbsrc.ac.uk
Class: shotgun.
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/clone="28a07"
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                                                                                                                                           Rhizobiaceae; Rhizobium.
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Matches 98; Conservative
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University of Washington 401 october 100 o
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Adb_xref="texon:9606"
/Clone="plate=1128 Col=13 Row=A"
/Clone_11b="RPCI-11 Human Male BAC Library"
/Clone_11b="RPCI-11 Human Male BAC Library"
/Note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Contact: Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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50.8%; Pred. No. 2.4;
tive 0; Mismatches 87;
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                                                                                                                                                                        Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
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Location/Qualifiers
1. .391
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Query Match
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Plate: 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffreden, M.D., NIH" 128 c 172 g 139 t 2.Others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    490 CAATTTACATGGCTGCACATCGGGTTAGGTTCTTTTCATCGCGCACATCAGGCGTGGTAT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   487 CACTICGCATATITACTCTTGGCTAAACCTTCATIGAAACACGAAAGACTGTCGTAGTAT 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             550 CTACACCGTTTGCAGGTGATGGGCGATAAACGCTGGAGCATTGCTGCGGGGAATATTCGT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 632;
                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:4950904"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                               found through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.gov
Plate: LLAM10906 row: e column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse BAC End Sequences from Library RPCI<sub>7</sub>23
Unpublished (1999)
Other_GSSs: RPCI-23-460F24.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37.6; DB 13;
Pred. No. 3.7;
DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                      High quality sequence stop: 322.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   /strain="FVB/N"
/db_xref="taxon:10090"
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1 Similarity 54.5%;
73; Conservative
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AZ115205/c
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
CCORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
161 c 129 g 186 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web: www.genoscope.cns.fr she i www.genoscope.cns.fr she i www.genoscope.cns.fr she i was grant of a collaboration of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogastar BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN03M07 of DrosBAC library from Drosophila melanogaster (fruit
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 787)
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/db_xref="taxon:7227"
/clone="BACN03M07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17;
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Pred. No. 4.8;
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                                                                                                              /organism="Mus musculus"
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                                                                                                                                                                                             /clone="RPCI-23-460F24"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
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                                                                                                                                                                   /db_xref="taxon:10090"
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/plasmid="pBeloBAC11"
                                                    Location/Qualifiers
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                                                                                                                                           /strain="C57BL/6J
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63.3%;
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Direct Submission
                                                                              .624
Seq primer: T7
Class: BAC ends
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Length 550;

DB 12;

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Query Match
Best Local Similarity
Matches 70; Conservat
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AUTHORS
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/organism="Zea mays"
/db_xref="db627:618047B01.y1"
/db_xref="looper:corrections of the corrections o
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                                                                                                                                             1411 ACGGAAGATGTCATTCCTTGCGTTGGGCGATAACGGTATCGATTTGCCAACCTACCGTGAT 1470
                                                                                                                                                                                                                                                                                                                                                                                     1591 GGCGTTCGCCCGAATGCCACCGCCATGTTACCTGCACTGTTTACGTATTCATGGAGCAG 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1531 GATGGTTTCTCGAAAATTCCGGCGATGATTGCCCCCACACTGCGAGGGGGGTGCTACCAGCGA 1590
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clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                        608 MKNMKTMNNMMNNMNNKNNNNNNNMMCMKKNNNCTKNMKNNKMNNMMKNNNMMMTMN 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       668 INCMNMKANTMMNKMMCMINMMINTINKININMMINMMNNMMINMINMMINKINKGMIK 727
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1651 TGGCATCACGGCAAACTGCCCTATGAATATCAGGATGCCATCCTTGATGCACCAGCT 1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                                                                                                                                                                                                                             548 NTMNNMKNNKKNKKNKMMKNNNTMNAMKNKKMKMNNNNMMMKMNKKNNNNNNN
                                                                                      ;
0
                           Length 787;
                                                                                      Indels
                     Ouery Match 2.0%; Score 36.6; DB 17;
Best Local Similarity 3.4%; Pred. No. 8.4;
Matches 12; Conservative 114; Mismatches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
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Plate: 1000205 row: G column: 12.
Location/Qualifiers
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BG268636.1 GI:12973751
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Walbot, V.
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AW165487 581 bp mRNA linear EST 10-NOV-19:
618047B01.x1 618 - Inbred Tassel cDNA Library Zea mays CDNA, mRNA
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Inbred tassel library from Schmidt lab"
148 c 109 g 188 t
                                                                                         981 CCATAATGGTGAACGTTTCCATGATGGCCTGGTTGAGTTTCTCCCAGCTAACTGGCAAACA 1040
                                                                                                                                                                                   1041 GGATGTCATCGACTGGCTGAGTACAAATACCACTTGCCCGAATACCATGGTTGACCGCAT 1100
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                                                                                                                    403 GGATATCTACACCCGGGATTTCTCTGAGCCCACTGGAGAAAGATGGATAAGAGGCAT 344
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/cultivar="Obio43"
/bb xref="taxon.4577"
/clone_lib="618 - Inbred Tassel cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="tassel"
/dev_stage="tassel length from 0.1 to 2.5 cm"
/lab_host="XLOLR"
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Unpublished (1999)
Contact: Walbot V
Department of Blological Sciences
Stanford University
Tel: 650 723 227
Fax: 650 725 8221
Score 36.4; DB pred. No. 8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36.4; DI
Pred. No. 8.2;
0; Mismatches
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Plate: 618047 row: B column:
    Location/Qualifiers
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2.0%;
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Best Local Similarity 55.6%;
Matches 70; Conservative
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Umansky,L., Heidthan,M., Nelson,K., Iwasaki,H., Kanada,D., Lugo,R.,
Hager,K., Miller,P., Roeder,G.S. and Snyder,M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
Gene Disruption
Unpublished (1999)
Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Fat: 203 432 9949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; 2ea.
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
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                                                                                                                                                                                                                        Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
Class: transposon-tagged.
Location/Qualifiers
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Zea mays CL67890_1 mRNA sequence.
AY110366
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Unpublished (2002)
2 (bases 1 to 791)
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 771)
Ross Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R.,
                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; 2ea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/cultivar="Ohio43"
/db_xref="taxon:4577"
/dbo_lib="tassel"
/tissue_type="tassel"
/dev_stage="tassel"
/lab_host="xLOLR"
/note="Organ: tassel; Vector: pAD-GAL4-2.1 (Hybrizap);
Inbred tassel library from Schmidt lab"
a 106 c 189 g 105 t __2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               981 CCATAATGGTGAACGTTTCCATGATGGCCTGGTTGAGTTTCTCCAGGCTAACTGGCAAACA 1040
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Walbot,V.
Malze ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                  Department of Biological Sciences
Stanford University
SSS California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
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Location/Qualifiers
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                                                                                                                                               GI:6431783
                                                                                                                                                                                                                                                                                                                                           University
Unpublished (1999)
Contact: Walbot V
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AZ163357
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/clone="Plate=73 Col=20 Row=B",
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urchin, sperm apenomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
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Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea: Echinodea; Echinoide;
Echinoidea; Euchinoidea: Echinodea;
Strongylocentrotus.

(bases 1 to 533)
Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Blondi,T.R.,
Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray
GAA., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. and
                                                                                                                   Jote-files sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project 129 230 t 85 others
                                                                                                                                                                                                                                                                                                                                                                                                                        981 CCATAATGGTGAACGTTTCCATGATGGCCTGGTTGAGTTTCTCCAGCTAACTGGCAAACA 1040
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/db_xref="MaizeDB:632757" |
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Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
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55.6%; Pred. No. 9.8;
tive 0; Mismatches 56; Indels 0
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California Institute of Technology
Pasadena California 91125, USA
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Class: BAC ends
High quality sequence stop: 533.
Location/Qualifiers
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Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 73 row: B column: 20
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Job time : 2848.31 secs
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                                                                    Best Local Similarity 48.1
Matches 99; Conservative
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March 21, 2003, 11:06:57; Search time 11422.3 Seconds (without alignments) 10117.650 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                    Sciences, University
GA 30602, USA
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vectors in E. coll
Plant Cell Rep. 20, 338-342 (2001) |
2 (bases 1 to 3971) |
LaFayette, P.R. and Parrott, W.A.
Direct Submission
Submitted (26-JUL-2000) Crop and Soil Sciences
Georgia, Plant Sciences Bidg., Athens, GA
                                                                                                                                                      coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1100.0%; Score 3971;
11arity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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AUTHORS
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q _Q	Oy 2 Dp 2	Qy 2 Db 2	Oy 2 Db 2		Qy 2 Db 2	Oy Dp 5	Oy 2 Db 2		Oy 2	Qy 2 Db 2	Oy 2 Dp 2	Oy 2 Dp 2	Oy 3			oy 3 Db 3	Oy 3 Dp 3	0y 3
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	CGCGCCACCGAACAAGCAGAGGGAATCAATGCCACCTCACCATCCGGTGCTGAACTACGTC 126	GGTGGTAAAATTTCGCCTGAAATGGAAACACCGAAAATTCTCTGGCTGAAAGAAA	CCAGAGAICTACGAACGTGCCGGACAATTTTCGAICTGGCCGATTTTCTGACCTGGCGG 138	GCTACCGGTGATTTAGCGCGTTCAGTATGCACTGTTACCTGTAAATGGACGTGGCTGGC	CATGAAAATGGCTGGGATCCAGATTATTTCCGCACCATTGGCCTTGCAGAGTTAGCGGAT 1500		TTAACAGCACAAGCGGCGGCAGAGGGATTACTCCCCGGCACACCTGTCGCTGTAGGG 1. 	TTAATTGATGCTCACGCTGGCATCGGTACGGTTGGCGTAGAAGGTGGACCCCTCAAC 168		TTTGTACCGGGTGTCTGGGGGCCGTATTACAGTGCGATGGTTCCAGGTCTGTGGTTAGTT 180	GAAGGCGGCAAAGTGCTGCGGAGCAGCTATTGACCAGCTACTTGATTTCCATCCGGCT 186		GATCGAATCCTCGAAAAAACGGCGCAACCATCAGATGCTGTCGCCCTGGCGAAAGGGCTA	CACGTGGTGCCGGAATTTCTCGGAAATCGCGCCCCTTCGCAGATCCTCATGCCAGAGCG 204	GTAATTIGIGGCCTGGGTATGGAGCGAGATCTGGATAATTTACTCGCCTTGTATATCGCT 2100	GGATTATGCGGAATTGGTTATGGTCTGCGCCAAATTCTCGACGCTCAAACACGCGCAGGGA 2160 	GTAGTGA GTAGTGA	
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TCGCCCATTCTTGGTGCTGTCGCCGGAAATATTGCACCTTCTGTTGGCGAAGCG CTGGGGTAGTAGCGGAAATCATCACGCCGCAAAAAACCATGCTGATTGGTTTTG TTCTCTCCAGTATTGTGCGCATTATAAATACCTTATCGTTATTCGGTTTTGCGG TGCCAATGATGTTGTGGATGAACTGGGATTCACCACCTCTGAATGGTTGCAGG CGGAGTGCATTCATCTGCACCCTAAAAACGAGGTTTATATGTCCAGAAATAATA GGTTGGGTTTGCCACTGCATCTGATAGGGGATATATCGCCATCGCAGTATTA GTGATGGTTTCGAACTCGCATTCTTATCGCACTATTTAAATCGTTAGGCTTCA GCAGATACCTGCGGTATTCCGGTCATTACCACGCAATGCTGCGAACCGGTTTTA CGTCGATATGAGGCCTATAAGCAGTTGCAGCATACTGCAAAATTACTCAGAGAC GGTTGGGTTTGCCACTGCATCTGATATGGGGATATATCGCCATCGCAGTATTTA GTGATGGTTTCGAACTCGCATTCTTATCGCACTATATAAATCGTTAGGCTTCA PCCTGCTGTTTTACGGGATTCGTGGTTTAGCGTATCCGCTATTTCTCTACTCAT TCGTTATTATTCATAACGTGCGTAGCGAAAATTCCAGTTCTGCTCTGGGTTGGT CAATTCACCCATGTGGATAATATTATTATCCGCAAGAACGCTATCAATCTCTT

Match 100.0%:	Best Local Similarity 100.0%; Pred Matches 3971; Conservative 0; Mi	п,	DD 1 ATCGATTGACAGGTTGCTTCACAGGGCCQCCCCCCCCCCC	121	121	Db 181 TGCAATGTGCAAAACGCTGGTGGATGC7 Qy 241 GCGACAAACTGCACAAGATTGTCGCTGAC Db 241 GCGACAAACTGCACAAGATTGTGGTGA	301	361	361	Db 421 ATCCAGATGTCTGGGATCGTGTTAAAA Qy 481 GTGCAGTCCTGCGCATATGATTGGGCAC	541		Db 661 TGCTGCCAGGACCAGTAGTCACTGCCCTC Qy 721 AAGCCCTGGCAAATGGTAGCTGATGCAF	781	Qy 841 ATCTGTAAGGGGGGAATCATGACAATAAAC 	Db 901 GCAGTGTCCGCGCGGGATTTTGATCT	
3361 TCTGGGCGCATTTTCTTTACCACTATTTTCTCTAAPATTTTTGGGGGATTGTGGGCAG 3420	TCTGGGCGGCATTTTCTTTACCACTATTTTCTCTAATATTTTTTGGGGGATTGTGGGCAA	3421 AAAAATGGGCTGGATGCGTGTTATTCGCTGGTTTGGTTGCTCGGGATGGCAGCATCAA 3480 	3481 GTTTAGCGTTTTACTACATGCCGCAATACTTTGGTCACAACTACTGGATGGCAATGATTC 3540 	3541 CGGCGATTGCTCTGGGAACTTTTGTTGCTGCTGATTGTGCCGATGGCCGCTGTCTTCCCGG 3600 	3601 CACTGGAACCAAAACACAAAGGTGCTGCAATCTCGGTT [†] ACAACCTCTGCGGGTATGT 3660 	3661 CTAACTTCCTGGCTCCGGCAATTGCCGTGGTGTTATTACCGTGGTTTAGCACTATCGGTG 3720 	3721 TGGTCATTGCCTATACAGCATTGTATTGGCCTTTGTCCTTTGCGCATTCATT	3781 TIGAGCAGCCAGGATTCAGTTCTGCGCCAGTGACTGAGAGGGCATTGAATATCTCCTGAA 3840 	3841 AAACGAAACGCATCAGCACTCATCCTCCTCATGGGAGAGGATTTCACATCAGG 3900 	3901 CAATAGTGACTTTGTTATCGAGATAAACGTCCTGCACGGCGTTAATCAGTTTCAGGCCGT 3960 	3961 CAGCCATCGAT 3971 	AX268027 AX268027 AX268027 LOCUS DEFINITION Sequence 2 from Patent W00166779. ACCESSION AX268027.1 GI:16516560	KERWOKUS SOURCE Escherichia coli. ORGANISM Escherichia coli Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.	REFERENCE 1 AUTHORS Parrott, W., Lafayette, P. and Kane, P. TITLE Arabitol or ribitol as positive selectable markers JOURNAL Patent: WO 0166779-A 2 13-5EP-2001; University of Georgia Research Foundation, Inc. (US)	EATURES Location/Qualifiers 1 source 13971 / organism="Escherichia coli" / /db_xref="taxon:562"	misc_feature 96. 848 /note="ribitol dehydrogenase coding region" misc_feature 859. 2463 /note="ribitol kinase coding region"	model finding particle and the control of the contr

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g å	08	AGGCAGTCTGTTCATTCGTAATGCGCTCACTCTGGCAGACGTTTGTGCACAAAGT 108 TGGCAGGCATCGGTTTTGATGCCACCTGTTCTCTGGTGGTACTGGATAAAAACGGTGT 114	
9 è	1141	3GCAGGCTGTCAGCCCGGAAGGAGGTGCAAAATATCATTGTGTGGATGAAATATGCCTGTCAGCCGGAAGAATGGAATGCATTGTGTGTG	
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oy O	1381	GCTACCGGTGATTTAGCGCGTTCAGTATGCACTGTTACCTGTAAATĠGACGTGGCTGGCA 1440 	
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ογ	1561	AGCACAAGCCGCGGCAGAGATGGGATTACTCCCCGGCACACCTGTCGCTGTAGGG 162	
СP	1561	THAMCAGCACACAGGCGCGCGCGCAGGCGATACTCCCCGGCACACCTGTCGCTGTAGGG 1620	
oy Op	1621 1621	TTAATTGATGCTCACGCTGGTGCCATCGGTACGCTTGGCGTAGAAGGTGGACGCTGAAC 1680 	
<u>ک</u> و	1681	TTCTCCCTCG 17	
3 8	74	-GO-GO-GRANDEN GO	
2 6	74	TITETACCOGGGGGCCGTATTACAGTGCGATGCTTCCAGGGGTGTGGTTAGTT 1800 TITGTACCGGGGGTGTCTGGGGGCCGTATTACAGTGCTTCCAGGGTCTGTGGGTTAGTT 1800	
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D Q	1981	CACGTGGTGCCGGAATTTCTCGGAAATCGCGCCCCTTCGCAGATCCTCATGCCAGAGCG 2040	
ò	2041	10	
2	4	TAATTIGIGGCCIGGGIAIGGAGCGAGAICIGGAIAATITACICGCCTIGTATAT	

Qy Db	2101	GGATTATGCGGAATTGGTTATGGTCTGCGCCAAATTCTCGACGCTCAAACAGCGCAGGGA 2160
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qa	2221	8 8
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Qy	2701	o o
Qy	2761 2761	
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TLLYTNRSILESSIVRIINTLSLEGFAVIMPMMFVDELGETTSEWLOVWAAFFETTIE
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1950 c 972 g 736 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               745 TGCAACCGATTGAAGTGGCGGAATCAGTATTGTTTATGGTGACCCGCTCGAAAAATGTCA 804
                                                  2 (bases 1 to 3233)
Heuel,H., Shakeri-Garakani,A., Turgut,S. and Lengeler,J.W.
Genes for D-arabinitol and ribitol catabolism from Klebsiella
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Submitted (29-JAN-1998) Biology, University of Osnabrueck,
Barbarastr. 11, Osnabrueck, NS 49076, Germany
On Feb 23, 1998 this sequence version replaced g1:2735582.
Location/Qualifiers
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Microbiology 144 (Pt 6), 1631-1639 (1998)
98304087
J. Bacteriol. 179 (19), 6014-6019 (1997)
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Heuel, H. and Turgut, S.
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Klebsiella pneumoniae
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Klebsiella.
1 (bases 1 to 3233)
Heuel, H., Turgut, S., Schmid, K. and Lengeler, J.W.
Substrate recognition domains as revealed by active hybrids between the D-arabinitol and ribitol transporters; from Klebsiella pneumoniae
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ALUUY/31 10789 bp DNA ' linear BCT 28-DEC-2001 Brucella melitensis strain 16M chromosome II, section 93 of 107 of

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Kapatral, V., Los, T., Ivanova, N., Anderson, I., Bhattacharyya, A., Lykidis, A., Reznik, G., Jablonski, L., Larsen, N., D'Souza, M., Bernal, A., Mazur, M., Goltsman, E., Selkov, E., Haselkorn, R., Fyrptdes, N. and Overbeek, R. Direct Submission Submitted (13-NOV-2001) Integrated Genomics, Inc., 2201 W. Campbell Park Drive, IL 60012, USA (bases 1 to 10789)
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SRSTYYNWVKAVREHRDITLDVDVLMRLSAVLGIHQALGVLYPGEAAGRKWLHTPNGA
SLFGGQPPLQLVASGTQDGLMAVRRFLDAARGGLXMEPKALDRAFHPYHDEDVVFS"
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
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Submitted (13.NOV-2001) Unite de Recherche en Biologie Molecul
Laboratoire d'Immunologie et de Microbiologie, Universite of to for true de Bruxelles, Namur 5000, Belgium
6 (bases 1 to 10789)
7 O'Callaghan, D.
8 O'Callaghan, D.
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Blzer, P. H. and Hagius, S. Direct Submission (13-NOV-2001) Department of Veterinary Science, L. Submitted (13-NOV-2001) Department of Veterinary Science, L. Center, 111 Dalrymple Building, Baton Rouge, LA 70803, USA (bases 1 to 10789)
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/gene="BMEII0977"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="II"
105. .581
                                                                                          AE009731.1 GI:17985189
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complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 10789)
                                                                                                                                                                                               Brucella melitensis.
                                          AE00891
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PROGRAMMENT TO THE TRANS A STATE OF THE TRANS A STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVŠASRŪPEBERETĀETĪLISYAIDELFICGATDPDGLHELCEKĀALPHVNIDLPGSRA
PSYTTDNFRAGGKMLTPAIIEYGEBEAPLOPBDLCLEGGRUDBESTRQKICGFHQVKQTV
LGADPEGCVETGYSATMIVALNDYRARHGRLPRGLFVNSSINLEGILIFFMAEHPGE
PLNDIVIGCYDYDPPASFLPFPVISILQDVEGMIAKAFDLMERRVTEPELHLIMPKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILQLADQHAYTANRQAQGLRHSRSGLVGLLLPLHDNRFFSAMAQIFEAHVRARSFCPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3713 CTCAATGGAAGAGTTGCAGCTGTAACGGGTGCTGCCTCCGGTATCGGCTTTGAATGTGCA 3654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3653 AAGCATATGATTGGGGCGGGCATAACCGTGTTTCTTGTCGACGCGACGAGAACGCGCTT 3594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3593 GCGGAAAAGTGCGTTGAGCTTGGCGACAAGGCCAAACCGCTGGTCGTCGATCTGCTCGAT 3534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 CTTAATGGCAAAGTTGCAGCTATCACTGGCGCTGCGTCAGGTATTGGCCTGCAATGTGCA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 CACAAGATTGTCGCTGAGTTAGGCGAAAACGCGTACGCGCTGCAACTCGATCTCTTCAAT
                                                                                                                                                                                                                                                 /product="D-GALACTOSE-BINDING PERIPLASMIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(7873. .8928)
/gene="BMEI10985"
complement(7873. .8928)
/gene="BMEI10985"
/codon_start=1
/transl_table=11
/product="RIBITOL OPERON REPRESSOR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="TRANSCRIPTION REGULATOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 824.8; DB 1;
Pred. No. 3.8e-230;
0; Mismatches 887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="BMEI10986"
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/codon_ct=
                              complement(6420. .7457)
/gene="BMEII0983"
                                                                                                     complement(6420. .7457)
/gene="BMEI10983"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7471. .7692
/gene="BMEII0984"
7471. .7692
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/transl_table=11
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                                                                                                                                                                                                                       /transl_table=11
   OHDNAHGRGEVR'
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                                                                                                                                                                                                                                                                                   PRECURSOR"
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Matches 1416; Conservative
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FVRIGTDVRAGGENLGGLSKQAAAELGLRFGTAIAAGLIDAHAGGIGTVGARGSEGRI
LSRWAYVEGTSACTWTTTEQPYFVDGWRPYFSAMVPGLWLNEGGQSAAGAAIDHLIH
PRAARAERKAAADADSLAABSLAABVABCGPEKŢAMIVGDIHVVPEFLGNRAFAD
PDARAVIAGLDLDTGWGSLAALYLAGLCGLGYGVRÒIIEAQRAKGITYDTIVVSGGAA
RSNLVRQVLADATGLUVTASTSPEPVLLGSAMLGAVASGAYPDLVTAWQVMSELGARN
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LGIATVFQDLALCENLDVVANIFLGREISPYRLDEVSMEIKAWKLLNELSARIPSVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MGATMTNYYLGVDVGTGSARAĞLFDAGGTMLASARRDIAIWREA
GGIVEQSSDDIWQAVCESVREVVRVAGVDPAAVAGİGYDATCSLVVLGEGGKPLAVGP
SNDRARNIIVWMDHRAGEQAERINTTRADVLGYVGGAISPEMETPKLLMLKEHKPETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEKCVELGDKAKPLVVÖLLDPASVATMMPQILEQAGQLDIFHANAGSYIGGPLWEGDP
DANDRALLININAARRTVHAVLPHMWERKTGDIIMTSSYAGVVPVIWEDIYTASKHAV
OARVHTVRQVAPHGIRVGGVLPGPVYTALISDWPQAKLDEALAAGSLMEPKEVAESV
MFMLTRPRNIIIRDLVILPQSLDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVGVAIIAALCAGALAGFLYALLYNRFSMPSFYSTLAGLLAALGLQLYLLGNTGSINL
PYGSWLVSFGQLLVMPRPLSYALALVAGLAIFFTGFRAAQRRRTAGLSAPSAAGIALK
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IEVAHHMRREAVATGIARLARTFRTYTARLEGSFVDISGEKETMADIYDHTSYAASQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MAQDLNGRVAAVTGAASGIGFECAKHMIGAGITVFLVDRDENAL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRAGINVNFIYVSAFMACSTLAAAGGIMAAARLASSSQQAGTGDVNLNAIAAAVIGGT
SLFGGRGSAWSALLGIIVIQSIASGLTLLDLSSSLRYMITGAVLAIAVIVDSLARRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MRHILLYARESEIMSQDHKAAATSSQPVLRLSGISKNFGAVSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVASLSGGQRQTVAISRSLLLDPKLIMLDEPTAALGVAQTAEVLDLIERVRDRGLGVI
MISHNMEDVRAVADRIVVLRLGCNNGIFYPDSSNEELVAAITGATSNSVSRRAERRLA
                                                                                                                                                                             FGEEMRATGETGILFDSLRHEGGINAVAFRPSRILEVTQADHYEITVEASSRRIEARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="GALACTOSIDE TRANSPORT ATP-BINDING PROTEIN MGLA"
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/db_xref="GI:17985195"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="RIBITOL 2-DEHYDROGENASE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPDARRAKWHDHRFEAFWLLQATARKIRYL"
complement(2997. .3725)
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/protein_id="AAL54221.1"
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/db_xref="GI:17985193"
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/EC_numher="?
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/codon etail
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/gene="BMEII0982"
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/gene="BMEII0981"
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/gene="BMEII0982"
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us-09-802-208b-2.rge

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372	432	492 3353	552 3293	612	672 3173	732	792 3053	852	912	972 2877	1032	1092 2757	1152	1212 2637	1272	1332	1392	1452

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BCT 30-AUG-2001

AF045245
Klebsiella pneumoniae D-arabinitol transporter (dalT),
D-xylulose-kinase (dalK), D-arabinitol dehydrogenase (dalD), and

RESULT 5 AF045245/c LOCUS DEFINITION

us-09-802-208b-2.rge

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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPSFTIPHIGEMGTLWIALAFCLTGGVIALVSLRHIGTPROHMONLTTERKFSELGRAA
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                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heuel. H. and Turgut. S.

Direct Submission
Submitsed (29-JAN-1998) Biology, University of Osnabrueck,
Barbarastr. 11, Osnabrueck, NS 49976, Germany
On Feb 23, 1998 this sequence version replaced g1:2735580.
Location/Qualifiers
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repressor (dalR) genes, complete cds.
AF045245 U97126
AF045245.1 GI:2905644
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Klebsiella pneumoniae
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                     ACCESSION
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KEYWORDS
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Pred. No. 4.6e-217;
0; Mismatches 298; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                        4816. .5757
/gene="dalR"
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Best Local Similarity 76.3%;
Matches 959; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            4816. .5757
/gene="dalR"
                                                                                                                                                                                                                                                                                                                  YTLIN"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLGLIGLYLRHAABETPAFTERLQRAEEBDRQSLKERPMVPIAEIAREHFRSLAICIG
MYLVYINVTYYYYYNLLTYMPTYLSKTLMYSEDHGYLIIAWWGMLFVQPAIGLLSDRIGR
KPFLAAGSTAILFLSLDAFHLIASGOVVQIFFGLLIIAWACMLIGIMASTLPALFPA
RIPKSALAIAFRISIIVIAGITPTVTAMLNEVYENIYMPAYLJMAAVEGIVTFFEKE
TANRPLYGDTPNASSRKEAKSLLAEQYQHIEKSVEEIDEELAKLEEGKKILQTKREGE
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ERDIIVWMHHAVEQARIINAGKHAVLKYVGGRISPEWQTPKLLMLSERRPDIYARAE
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GESVYHPGTALGNGITEBAARAMGIVAGTAVAAGLIDAHAGGVGTVAAGGDASRCLGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MVVRHSRGQQLNSQIQASPLSIDDVTVIDDDKVKKAVTAAALGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMEWFDFGVYGFVAXAVGKVFFPDAAPAVQTVAALATFSVPFLIRPLGGIFFGAMGDK
FGRQKVLSLTIIIMAASTFCIGLIPGYATIGIWAPILLLLCKLVQGFSVGGEYTGAAI
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CDELINSAGINVLESVLDADSDASTAVLGINLERAALVYCOGERRGRYANGGGALVNI
TSIACHRGFQDHLCYAASRAGLEGARFVLARELGPHGIRVNAVAPTITLTELAAEAWN
DPEKSQPMWVRHPLNRFAEAEEVAQSIALLLSDDSKMISGAVLPVDGGFLAV"
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                                                             (Cereon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PROLINE/BETAINE TRANSPORTER (PROLINE PORTER II)
  chromosome and 200 bp missing from the right end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3158, .4768)
/gene="AGR_L_1075"
/note="D-ribulokinase (EC 2.7.1.47) - Klebsiella
                                                             C58

    10295
/organism="Agrobacterium tumefaciens str.

                                                                                                                      complement(195. .704)
/gene="AGR_L_1070"
complement(195. .704)
/gene="AGR_L_1070"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2383. 3195)
/gene="AGR_L_1073"
/note="carbonyl reductase"
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                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="AGR_L_1071"
747. .2297
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                                                                                  /strain="C58
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                       FEATURES
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linear chromosome, section 56 of
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Hinkle,G., Slater,S.C. and Goodner,B.
Direct Submission
Submission
Submission
Submission
Submission
Approximately 800 bp of telomeric sequence missing from the left
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Agrobacterium tumefaciens str. C58 (Cereon)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                3200
                                                                                                                         1063
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HinkLe,G., Slater,S.C. and Goodner,B.
Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Gall Disease in Plants
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                         3141 TTGCGTCATGTTAAAACGCCTGGACATATGCATAATTTAACTCCCCGTGAGAAGTTTGCA
                                                                                                                                                                 GAATTAAGTCGGGCAGTAACTTTACTTTATACCGAACCGCAATATTTTCTCTCCAGTATT
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AE008252 AE007870
AE008252.1 GI:15158917
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FALLAKLGERAIPOYTNLLDADSCRAMIPEILGKUÖHIDILTCNAGTYIGGDLTETTP
EALDKMLINUNAVWKNVQAVVPHWSERKTGDIIVTCSIAGHFPTYWEPVYSGSKWAI
TSFVOGWRRQAIPHVRVAQVSPGFVVSALLADWPEENLRKAKESGSLIDASEVADAV
VYMLTRKRTVTIRDMLVLPTNFDRV"
complement (5629. 6612)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mmmsldbnrgvaaktggfsfsamlrsplalplaglivvsilmgl
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GVKTRRVKLAVYGISGVTAAFAALILTGRLMSGQPNAGVGFELDAIAAVULGGTAIAG
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EPTRGIDVGAKAEITSLEMPRAARGHSIIMISSELPEVIGMSDRVCVFRSGGIVATVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEALKEAAAS IGADVYTDAGHDVAKQI SDVEDMLQXKI DILLLINPTDSAGI IEBANHA
AKAAGVIVVAVDANANGPVDTFVGSKNRDAGÝKSCKHLGDALGGKGEVALLDGIPVP
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ROILADATGLPVELTECEEPVLLGSAMLGAVAAGTYPDLMAAMPAMSRIDSSAMPDPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(8170. .9081)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bermease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRGLILGTLIGAVLLGILNNGLNLMGINPYLQDVIKGGIILLAIYIGREWR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein of ABC transport system"
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complement(6596 .8014)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(8170. 9081)
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complement(8170. 9081)
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complement(4858. .5589)
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GQSPSAFSRAFKRHTGTTLVRYRNQLRIDLACQMLLADQDVKVAEVCYDVGFSNLSNF
NRHFLKLKGMSPSRFFTIFAAQKAANWAE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAACGTGCAGGCCGTCGTGCCGCACATGTCGGAGCGCAAGACCGGTGACATCATCGTC 5179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGAACTAAATGTCTGAATCGCTGCAAGGCAAGATCGCGGTCATCACCGGCGCCGCATCC 5539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTGCTCGATCGCCGGCCACTTTCCGACCTATTGGGAGCCGGTCTATTCGGGCTCGAAA 5119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410
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                                                        MtlR PA2337 (imported) PAO1)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGAAGGTGATCCAGATGTCTGGGATCGTGTTAAAATCTGAATATAAATGCGGCGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 10295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 643.2; DB 1;
Pred. No. 8.8e-177;
0; Mismatches 1003;
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Pseudomonas aeruginosa (strain
                                                                                                                                                                                                                                                                                                                                                                                              2031
                         .10096)
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16.2%;
Best Local Similarity 55.2%;
Matches 1331; Conservative
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7	CAACTTCGACCGCGTTTAATAATCTCTGGAGCGGGAAGAACCGGAAACGGTTCCGC 481	6
80	877	
æ	475	6
878T 758 ATCT	TTATTGGTGTTGATGTGGGATCAGGCAGTGTCCGCGCGGGGATTTTGATCTCACG 934	6
935 GATO 1 698 GCA	GATCTCTGCTATCCCATGCCACAGAAAATCACGACTGCGGGGGGGG	6
995 TGG 638 CCG	TGGAACAGTCCAGCCAGGAGATCTGGCAGGCGGTCTGT†CATGTATTCGTAATGCGCTCA 105. 	9 4
055 CTC 1 578 CAC	CTCTGGCAGACGTTTGTGCACAAAGTGTGGCAGCATCGGTTTTGATGCCACCTGTTCTC 111/1	4 6
115 TGC 518 TTC	TGGTGGTACTGGATAAAACGGTGATCCATTGCCTGTCAGCCCGGAAGGAGATGCAAAGC 1174 	4 6
175 AA4 458 GTC	AAAATATCATTGTGTGGATGGATCACCGGCCACCGAACÅAGCAGGGGGAATCAATGCCA 1234 	4 6
235 CT	CTCACCATCCGGTGCTGAACTACGTGGTAAAATTTGCCTGAAATGGAAACACGG 129, 1	4 0
295 AA 338 AG	AAATTCTCTGGCTGAAAGAAAATATGCCAGAGATCTACGAACGTGCGGACAATTTTCG 135, 	4 6
355 AT 278 AC	ATCTGGCCGATTTTCTGACCTGCGGGCTACCGGTGATTTAGCGCGCTTCAGTATGCACTG 1414 1 1 1 1 1 1 1 1	4 6
415 TT 218 TC	TTACCTGTAAATGGACGTGGCACATGAAAATCGCTGGGATCCAGATTATTTCCGCA 1474 	4 6
475 CC 158 AG	CCATTGGCCTTGCAGAGTTAGCGGATGAAGATTTTATTCGCTTTGGTCATCATATTGTTT 1534 	4 0
535 CT 098 AT	CTCCCGGAACACCTTGTGGAAATGGTTTAACAGCACAAGCGGGGGGGG	4 0
595 TC 18	TCCCGGCACACCTGTCGCTGTAGGGTTAATGATGATGCTCACGCTGGTGGCATCGGTACGG 165. 	4 6
655 TT 978 TC	TTGGGGTAGAAGGTGGAGGCGTGAACAATCTCGGGTATGTTTTCGGCACTTCTTCATGCA 1714 	4 6
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775 CG 858 CA	CGATGGTTCCAGGTCTGTGGTTAGTTGAAGGCGGCAAAGTG [†] TGCGGGAGCAGCTATTG 1834 	4 6
1835 AC 3798 AT	189 373	4 0

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Agrobacterium tumefaciens str. C58 (U. Washington).

Agrobacterium tumefaciens str. C58 (U. Washington)

Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;

Rhizobiaceae; Rhizobium.

1 (bases 1 to 11437)

Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E.,

Chen, Y., Woo, L., Kitajima, J.P., Okura, V.K., Almeida Jr., N.F.,

Zhou, Y., Bovee Sr., D., Chapman, P., Clendenning, Jr., Deatherage, G.,

Gillet, W., Grant, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M.,

MCClelland, E., Palmileri, A., Raymond, C., Rouse, G.,

Saephimmachak, C., Wu, Z., Gordon, D., Eisen, J.A., Paulsen, I.,

Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M.,

Krespan, W., Perry, M., Gordon-Kamm, B., Liao, L., Kim, S., Hendrick, C.,

Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.

The genome of the natural genetic engineer Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11437 bp DNA linear BCT 20-DEC-2001 sns str. C58 linear chromosome, section 130
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Wood,D.W., Setubal,J.C., Kaul,R., Monks,D., Chen,L., Wood,G.E.,
Chen,Y., Woo,L., Kitajima,J.P., Okura,V.K., Almeida Jr.,N.F.,
                                                                                                                                                                                                                                                                                                        2134
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                                                 3738 GCAAAGCATTGCCAGTCTGGCTTGCCGACCGCGCGCTCAGCCTCGCCGCATCCGCTTCCG 3679
                                                                                                                                                                                                                                                      3618 CCTTCGCCGATCCCCATGCTCGCGCCATCATTGCCGGTTATGGCATGGAGGGGGGGTGG 3559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3378 TGACCGAATGCGAGGAGCGGTGCTGCTTGATCTGCCATGCTCGGCGCCGTTGCGTG 3319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2195 CCGGGCAGCATCCACTGGTACGACAATTCTGGCAGATACCTGCGGTATTCCGGTCATTA 2254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2315 ATATTGCACCTTCTGTTGGCGAAGCGATGCAACAATTCACCCATGTGGATAAATATTATT 2374
1895 ATCAGCCCTCCCGTCTGGCTTGCTGATCGAATCCTCGAAAAACGGCGCAACCATCAG
                                                                                                                           3318 GAACCTATCGGACCTGATGGCTGCCATGCCGCGATGTCGCGTATCGACAGCAGTGCAA
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                                                                                                                                                                                                       CCTTCGCAGATCCTCATGCCAGAGCGGTAATTTGTGGCCTGGGTATGGAGCGAGATCTGG
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                                                                                                   1955 ATGCTGTCGCCCTGGCGAAAGGGCTACACGTGGTGCCGGAATTTCTCGGAAATCGCGCCC
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Science 294 (5550), 2317-2323 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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KEYWORDS
SOURCE
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OROLLIAAVSVLALLELLULANANSSAALAFAYFLSGYAISPYFITSGLIERRYPESM
LIEGYTWWWTGIGIGMAFGAFISGWVIDNFGPDNGFWVSVAASLTTVAIIGLGORSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MIAETRAKLLAAGRKAFGSIGYAEASMDDFTAGAGLTRGALYHH
STORKGLLAMAVVAEDDABWYRRLODISSAETRWEGFVEENVGYVRMALEPELORIMF
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IANSDDPETTSKRAVTSFRTFLEGLRIRKG"
Zhou,Y., Bovee Sr.,D., Chapman,P., Clendenning,J., Deatherage,G., Gillet,W., Grant,C., Guenthner,D., Kutyavin,T., Levy,R., Li,M., McClelland,E., Palmieri,A., Raymond,C., Rouse,G., Saenphimmachak,C., Wu,Z., Gordon,D., Eisen,J.A., Paulsen,I., Karp,P., Romero,P., Zhang,S., Yoo,H., Tao,Y., [Biddle,P., Jung,M., Krespan,W., Perry,M., Gordon Kamm,B., Liao,L., Kim,S., Hendrick,C., Zhao,Z., Dolan,M., Tingey,S.V., Tomb,J., Gordon,M.P., Olson,M.V.
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QAALRARIQPGDIAVVTGAGPIGMMVALAALAGGCAKVIVADLAQPKLDIIAAYDGIE
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PVDIVGLQAKELRVETVFRYANVYDRAVALIÅSGKVDLKPLISATIPFEDSIAGFDRA
                                                                                                                                                                                                                                          Direct Submission
Submitted (27-SEP-2001) Department of Microbiology, University of
Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
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located using Blastx/Glimmer" //odon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="ABC transporter, membrane spanning protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="transcriptional regulator, TetR family"
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                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Agrobacterium tumefaciens str. C58 (U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(68. .1297)
/gene="Atu4316"
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/gene="Atu4316"
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .11437
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/gene="Atu4317"
1441. .2013
/gene="Atu4317"
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/gene="Atu4319"
3670. .4569
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2261. .3313
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/gene="Atu4318"
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/trānslation-"MGGTMMQPDLELVHIRKGESFAAWRHGYPFRTVRWHYHPEYEIH
LIVVATSGFFYIGDEVGRFSSEQLIWTGPNLPQNWISEIEPDEIVPTRSLVIQFPESFI
EDACTSWABMOVRALLDRSRRGILFPDETSDRVRPLVLRLIEAQGIFRLALFWBILD
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FSRRPKRHTGTTLVRYRNQLRIDLACQMLLADQDVKVAEVCTDVGFSNLSNFNRFLK
LKGMSPSRFRIIFAAQKAAVMAE"
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ISSELPEVIGMSDRVCVFRSGGIVATVEGEDINSETIMTNATTGRVEHVA"
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KILCGILQPSEGTIRIDGKDRRFANYDEAIAAGVGIVFQEFSLIPYLNAVENMFLARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLDEPTATLTPSETEHLFNVMRELRRQGVAIIFISHHLDBIFEICDRITVLRDGELIG
SCLTSEVDNDRLVEMMVGRRIEASFPPKPQIDPSAAKVIEVEELQLKKGGPVSRFSLR
KGEILGFAGLVGSGRTETVLAMLGAHSASRRKIKLKLDGVDTRLSGPDDALMRGIGLLPE
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/note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
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[ribose]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="ABC transporter, substrate binding protein [ribose]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="ABC transporter, nucleotide binding/ATPase protein [ribose]"
                                                                                             /product="transcriptional regulator, AraC family"
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/db_xref="G1:17742785"
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/transl_table=11
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/franslation="MSESCALIDAS
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3RGLILGTLIGAVLLGILNNGLNLMGINPYLQDVIKGGIILLAIYIGREWR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity; putative;
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M25606.1 G1:149318
M25606.1 G1:149318
Tibitol dehydrogenase.
K.aerogenes DNA, clones lambda-[prbt,prbt.dal] and pJCW1.
Klebsiella aerogenes
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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 CGATGGTTCCAGGTCTGTGGTTAGTTGAAGGCGGGCAAAGTGCTGCGGGAGCAGCTATTG 1834
                                                  ACCAGCTACTTGATTTCCATCCGGCTGTTGAAGAAGCTCGCGAAATGGCACAACGTGTGA
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Loviny, T., Norton, P.M. and Hartley, B.S.
Ribitol dehydrogenase of Klebsiella aerogenes. Sequence
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1. .851
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28. .777
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TAASKRAVQARVHTRRQVAQYGVRGAAVLPGPVYTALLDDWFKAKMDEALANGSLMQP
IEVAESVLFMVTRSKNVYVRDIVILPNSVDL"
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                                                                                                                                                                    804. .>851
/note="ribitol dehydrogenase rbtK"
                                                                                                                                                                                                                                                                                                                                                                          Score 468.6; DB 1;
Pred. No. 1.3e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 184;
                                                                                                                                                                                                        /codon_start=1
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17.2 a 248 c 264 g 167 t
bp upstream of SalI site.
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(AL161576) putative protein [Arabidopsis thaliana]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deng,W., Burland,V., Plunkett,G. III, Boutin,A., Mayhew,G.F. Liss,P., Perna,N.T., Rose,D.J., Mau,B., Zhou,S., Schwartz,D. Fetherston,J.D., Lindler,L.E., Brubaker,R.R., Plana,G.V., Straley,S.C., McDonouph,K.A., Nilles,M.L., Matson,J.S., Genome Sequence of Yersinia pestis KIM
J. Bacteriol. 184 (16), 4601-4611 (2002)
                                                                                                                                                                                                                                                               linear
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of 415 o
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Submitted (21-FEB-2002) Genetics, U
Henry Mall, Madison, WI 53706, USA
Location/Qualiflers
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Yersinia pestis KIM section 23 c
AE013623 AE009952
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complement(728. .2380)
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ALVVLQLLESGLNLLGVSSYLTMALWGGVLILFIALQNRRA" RSPRANDNLTGITGLKLSTTPEDMALRYLATIOALALGTRHIIETMNONGYNIDTMM ASGGGTKNPIFVQEHNNATGCAMLLPEESEAMLLGSAMMGTVAAGVFESLPEAMAAMS RIGKTYPTPOTNKIKAYYDRKYRYFHQMYHDHMRYQALMQEGA" COMPLement (2384 . .3337) /gene="y0212" complement (2384 . .3337) SFEGSDGYDYGLTLPLLCLAGTIIFTGVMMNYTRLGRQIFAMGSNKDAASRLGINIFR LHLYYYGYBATLAGVAAVVQAJSQSYAPNSLMGFELTVLAAVVLGGTSMSGGRGSLT GTVLGVMLLAFLQNGLTLLGSVSSYWHTVFSGVIILVSISTTAWNEKRKLLREH" COMPLEMEDT (4321. .5817) NAAKIGATVKPMGAPLGHGLSQRAASEMGLIPGTAVSVSIIDAHAGTIGILGASGVTG ENANFDRRIALIGGTSTAHMAMSRSAHFISGIWGPYYSAILPEYWLNEGGQSATGALI DHIIQSHPCYPALLEQAKNKGETIYEALNYILRQMAGEPENIAFLTNDIHMLPYFHGN S /translation="MTQATAFITLENISKRFPGVLALDGVNLTLNKGEVHCLAGONGC GRYTITKVISGGYQPEKGASILIDGKLLHQLFPGLSFYGYGVJIXQDLSLFPNLTVAE GIASHTKYLPGGDFWYKKASHERALANGVGVTLDLDKKVEGLSIADROLVALCRAI AADARLVIMDEPTASLTSQEVKGLLNVRDLKSQGICVYFVSHRLDEVMEVADRISVM RDGKWYGTWQASELDSHELAFLMTGQRFTYRPLPPLAAKAAPLLEIRKLSRGEQFRNI DLTLHQGEIVSITGLLGAGRTELCLSLFGMTQPESGEIFVAGEPVRFRHNRDAIRHGI GYVSEDRLTQGLIMEQSIYDNTIVSVFDQLHTRSGLLDHSKAAALVNKLVQDLNIKVS /product-"putative permease of ABC transporter"
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to residues 16 to 306 of 318 from GenPept:
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component of transport system, probably ribose specific
[Escherichia coli 0157:H7 EDL933] component of transport system, probably ribose specific [Escherichia coli 0157:H7 EDL933]" /function="transport; transport of small molecules; /gene="y0234" /function="transport; transport of small molecules; complement(3339. .4328) /gene="y0233" complement(3339. .4328) complement(4321. .5817) /db_xref="GI:21956910" /codon_start=1 /transl_table=11 /transl_table=11 /transl_table=11 /codon_start=1 /gene="y0234"

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YDLLIQPALEDYPIDDEIAAASYMNKVIEKEIMRAPEQYLMHRRFKTRPIGEPSLY"
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                                                                                                                                                                                                                                                                                                                                                EDLIAKNVDAIIVVPNDAKVLEPVLKKAQEKGIVVLTHESPDÖRIGOMDVETTÖSEKY
AQARNDELEAKAMGNKGGYAITVGSLIVPLHNNMADYAKKYÖKEKYPENFEYPRELDVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                            carbohydrates, organic acids, alcohols"
/note="residues 25 to 350 of 352 are 53.37 pct identical to residues 5 to 37 of 328 from GenPept:
>9blaAG54669.1|AE005211_4 (AE005211) putative periplasmic binding protein, probable substrate ribose [Escherichia coli 0157:H7 EDL933]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pct identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="putative factor"
//note="residues 25 to 333 of 333 are 66.66 pct identical
/note="residues 25 to 337 of 328 from E. coli K12: B2378;
residues 28 to 333 of 333 are 66.66 pct identical to
residues 1 to 335 of 306 from GenPept: >emb(cAD07638.1)
(AL627274) putative acyltransferase [Salmonella enterica
subsp. enterica serovar Typhi]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAAACAATGGCAAGTTACTTTATCGGCGTAGACGTAGGGACCGGCAGTGCAAGAGCTGG 2313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to residues 18b to 247 of 431 are 26.15 to residues 515 to 579 of 865 from GenPept: >dbj|Bab73440.1| (APO03587) ORF_ID:all1741 probable proteinase [Nostoc sp. PCC 7120]" /codon_start=1 /transl_table=11
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Pred. No. 3.3e-96;
0; Mismatches 695; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative heat shock protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="unknown"
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to residues 515 to 579 of 865 from
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                                                /gene="y0235"
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7723. .8724
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1653 1097 2133 1157 2073 2013 1277 1457 1773 1517 1577 ----CTCGCGTATGTTTTCGGCACTTCTTCATGCACCATGGCATCTACCACTTCTCCCTC 1739 1800 TGAAGGCGGCCAAAGTGCTGCGGGAGCAGCTATTGACCAGCTACTTGATTTCCATCCGC 1859 1979 2039 1173 2012 GGAGCGGATTAATGCCACCAAGCACCCGGTCCTGGAGTTTGTCGGTGGTGTGATTTCGCC 1953 TGAAATGGAAACACCGAAAATTCTCTGGCTGAAAGAAAATATGCCAGAGATCTACGAACG 1337 1833 1637 1593 1592 TGGGACGATTGGCATTCTCGGTGCCAGTGGTGACGGGGGAAAATGCTAACTTTGATCG 1533 2040 GGTAATTTGTGGCCTGGGTATGGAGCGAGATCTGGATAATTTACTCGCCTTGTATATCGC 2099 AGAGCGAATCAATGCCACTCACCATCCGGTGCTGAACTACGTCGGTGGTAAAATTTCGCC GGCAGAGATGGGATTACTCCCCGGCACACCTGTCGCTGTAGGGTTAATTGATGCTCACGC ATCAGAAATGGGGTTGATCCCCGGTACGGCGCTCAGTGTCGATTATTGATGCTCACGC TGTTGAAGAAGCTCGCGAAATGGCACAACGTGTGAATCAGCCCCTCCCCGTCTGGCTTGC TCATATGTTGCCGTACTTCCACGGTAACCGCTCTCCCCGTGCCAAATCTGAATCTGAGGG TGATGCCACCTGTTCTCTGGTGGTACTGGATAAAAACGGTGATCCATTGCCTGTCAGCCC 2132 TGATGCGACTTGCTCGCTGGTGGTTTGGATAAAGAAGGAATCCACTGACGGTTAGCCC TCCAGATTATTTCCGCACCATTGGCCTTGCAGAGTTAGCGGATGAAGATTTTATTCGCAT TCCGTCCTACTTCAAATTGGTGGGGCTGGCCGATTTACTGGATAACAACGCGGCGAAGAT TGGTCATCATATTGTTCTCCCGGAACACCTTGTGGAAATGGTTTAACAGCACAAGCCGC 1712 CGGTGCGACGGTTAAACCCATGGGGCACCGTTAGGGCATGGTTTAAGTCAGCGGGCAGC GTTTGTACCGGGTGTCTGGGGGCCCGTATTACAGTGCGATGGTTCCAGGTCTGTGGTTAGT CTATCCGGCACTGCTGGAACAGGCTAAAAATAAGGGCGAAACCATCTATGAGGCGCTGAA TGATCGAATCCTCGAAAAAAGGGCGCAACCATCAGATGCTGTCGCCCTGGCGAAAGGGCT ACACGTGGTGCCGGAATTTCTCGGAAATCGCGCCCCCTTCGCAGATCCTCATGCCAGAGC <u> ACCCAAGGCTGATTTTGTTGAGCAGTCTTCCGAGAATATTTGGCAAGCGGTGTGTAATGC</u> TGCCGGACAATTTTTCGATCTGGCCGATTTTCTGACCTGGCGGGCTACCGGTGATTTAGC TGGTGGCATCGGTACGGTTGGCGTAGAAGGTGGAGCGCTGAACAAT - - -

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Similar to Escherichia coll VgrG protein TR:052672 (EMBL:AF044503) (713 aa) fasta scores: E(): 0, 49.9% id in 579 aa, and to Escherichia coll VgrE protein TR:052660 (EMBL:AF044499) (702 aa) fasta scores: E(): 0, 49.3% id in 576 aa. Similar to YpO3613 (78.0% identity in 803 aa overlap) and to YPO0764 (77.2% identity in 615 aa
                                                                 IESLALTLFRTHGVDLQTAVYYTLARTQKNGLAGFTEGCELLAGMVVGQWDHLMPEQP
OARSELLEMPRYRVSKQLFKQNBFTRDDLLAVYRERALAGLTDYKLQQYELKRVPRIEN
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HFSFIPHTQTWRPTPLAKPAMDGPQIAMVVGPPGEEIYCDEYGRIRLQFLWDRYGQSN
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SEHIGODOSVTVVRNOSNTIQNDRRVEVTRDQQTEVGNDYQLVVKGEKKEFVTKIRYT
EVHEDETLTVTKSIKIHAKGGDISISTPNAGITITHDGAIVLQGKYIRLAADMIDLNP
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                                                                                                                                                                                                                                                                                                                                                                /note="Similar to Arabidopsis thaliana F15P11.1 protein TR:Q9S9U2 (EMBL:AF160760) (187 aa) fasta scores: E(): 0.024, 31.5% id in 143 aa"
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/note="YP00154 E1-E2 ATPases phosphorylation site.
3038. 3103
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/protein_id="CAC93074.1"
/db_xref-"GI:15981526"
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/product="conserved hypothetical protein"
/protein_id="CAC93076.1"
   /db_xref="SPTREMBL:Q82B25"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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827. 1360
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/gene="YPO3606"
1382. .3784
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/gene="YPO3606"
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/gene="YPO3606"
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/gene="YPO3607"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCT 06-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Versinia pestis.
Yersinia pestis
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                           2159
                                                                                                                                                                            1053
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                                                                                                                                                                                                                                                                                                                                                                                                       2279
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Direct Submission
Submitted (04-0CT-2001) Submitted on behalf of the Yersinia Submitted (164-0CT-2001) Submitted (164-0CT-2001) Submitted (164-0CT-2001) Submitted (164-0CT-2001) Submitted (165-0CT-2001) Submit
1172 CATTATTACTGGCCTGAAACTCTCTACCACGCCAGAAGATATGGCGCTGCGTTATTTGGC
                                                                                                                                                 1052 CTATAACATCGACACTATGATGGCCAGCGGGGGCGCGGGGCACCAAGAACCCCATATTGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yersinia pestis strain C092 complete genome; segment 18/20
AJ414158 AL590842
AJ414158,1 GI:15981524
                                                                                                   2100 TGGATTATGCGGAATTGGTTATGGTCTGCGCCAAATTCTCGACGCTCAAACAGCGCAGGG
                                                                                                                                                                                                                                                 992 GGAGCATGCGAATGCGACGGGCTGCGCCATGCTGTTGCCAGAAGAGAGTGAGGCGATGCT
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_Location/Qualifiers
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/protein_id="CAC93073.1"
/db_xref="G1:15981525"
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48. .830
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on the World Wide Web.
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VERSION
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Best Local Sim.
Matches 814;
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/d
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ERDTYALSSPFETCF I FEAFSEAGVAKLASLEDLNGHALY FSYDDIGQLKKISTTSGY

ERDTYALSSPFETCF I FEAFSEAGVAKLASLEDLNGHALY FSYDDIGQLKKISTTSGY

GYVOVERGREKUSVAROVKGGTPETLLYRYQYNEDHOLVSYTNREGOITROFGYHGHLIN

KLADVGGLECRYTWADIGGPRITHTSTANLGEDWOFDYDIDNOGTTLTDLNTGGTACW

GYNAQHLITDYRADFOGGRYAPDYNDLMAPVAYAGERTUVYDALARPIOTIDPLK

RETHIDYHRNSLRVYRRQY PDGQVWKGEYDRTGRLLKENAPDGGVTLYYP FGASSLPE

RIANYGAGHLGGOLFBHTDCSGKLTRYEYDIOGHLLYVIDARNHSTHYSYNR

IGOPTGIRYADGRKEOLLYNAQGLYGPTDPVGRQLHWRYNLRGGPVSFTDRLQREYR

YRYDCHQMIELDNAMOGGYHFRWSSGGQLYGPRYQRHWRYNLRGGPVSFTDRLQREYR

PTVDDLTVSRQVSEDYDAGGRATQRLTGMSATRYDWDIMDRLLLAERRVPTAVGEGGGT
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FHTDINGTPLDVTDCEGKHWKGKYHAWGKYTRQNVSDPROSTVSRFAQPLRYPGQVS
DDFTGLHYNTFRYYDEIGRFSTQDPIGLAGGINLYQYGPNPLTWIDPWGWAFGGVDF
TGSPDLFPVKGSQLMIVETTWGARGNBFTBAFKLAGISKADATGYWHHLNDFDPVS
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VWQRQVALOVGDHMMIFTATNASPFNPQQOATWEQWIHSFAPWAREAGHV"
4241. 7105
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LTDSRERHQLSVAEDFAYDNADNLLNLRKLPFÖTVDPLYDTPVANNRLTQWQHYRFEY
DAWGNMTTRHAGGRMQHFAYDDDNRLLRAWGTGPLGEHDSHYRYDALGRRIHKSVTIK
                                                                                                                                                                                                                                                                /note="Similar to Escherichia coli CorE protein TR:052666 (EMBL:AF044501) (1420 aa) fasta scores: E(): 8.3e-32, 27.7% id in 824 aa, and to Escherichia coli RhsD protein Procursor SW:RHSD_ECOLI (P16919) (1426 aa) fasta scores: E(): 1.4e-28, 27.3% id in 842 aa"
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AAAGYGLEKGVGAIAGYFGYPVDVISGQKLLTGEGDDTDFILPGIFPLHWSRIYRSEN
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HAGDTLISBESRDNLHREVSRTQGILTQYRDYDÄMGRRL"
4298 - 4366
/gene="YPO3608"
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protein RhsD TR.AAA24544 (EMBL:L19084) (1426 aa) fasta
scores: E(): 4.6e-14, 28.33 id in,473 aa, and to
Escherichia coli RhsE protein SW.RHSE_ECOLI (P24211) (682
aa) fasta scores: E(): 1.6e-14, 26.88 id in 5.2 aa"
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for Ypo3608 by TMHMM2.0"
4385. 4453
4385. 4453
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for YPO3608 by TMHMM2.0"
7133. .8503
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/gene="YPO3609"
7133. .8503
                                                                                                                                /gene="YPO3608"
/4241. 7105
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/gene="YPO3610"
8505. Room
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/gene="YPO3609"
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/gene="YPO3610"
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/note="Similar to Bacillus subtilis Yokk protein TR:031996 (EMBL:299115) (192 aa) fasta scores: E(): 0.043, 26.6% id in 154 aa, and to Bacteriophage SPBc2 hypothetical protein Yokk TR:064025 (EMBL:AF020713) (192 aa) fasta scores: E(): /codon_start=1 //codon_start=1 //transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 858 CATGACAATAACCAAAAACCGTTATTGGTGTTGATGTGGGATCAGGCAGTGTCCGCCCGG
                                                                                                                                                                                                                                                                                                                                                918 GATTTTTGATCTCAACGGATCTCTGCTATCCCATGCCACGAAAAAATCACGACTACGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                   978 GCGCAGCGGAAGCCGCGTGGAACAGTCCAGCCAGGAGATCTGGCAGGCGGTCTGTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGATGCCACCTGTTCTCTGGTGGTACTGGATAAAAACGGTGATCCATTGCCTGTCAGCCC
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                                                                                                                                                                        Length 235050;
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                                                                                                                                                                          Score 369; DB 1;
Pred. No. 4.8e-96;
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Submitted (01-OCT-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC014947 1923 bp mRNA! linear PRI 04-OCT-2
Homo sapiens, clone MGC:22958 IMAGE:4871664, mRNA, complete cds.
BC014947
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Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
                                                                                                                                                                                                                                                                                                                          43007
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                   42948 TIATATTTTGCGTCAGATGGCGGGTGAACTGAAAATATCGCGTTCCTGACGAAGATGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTATAACATCGACACTATGATGGCCAGCGGAGGCACCAAGAACCCCATATTTTTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43308 GTTGGGGAGTGCCATGATGGGTACCGTCGCTGCGGGGTGTTTGAGTCATTGCCGGAAGC
                    42768 CITTATCAGTGGTATTTGGGGGCCATATTATTCGGCCATTTTACCGGAATATTGGTTGAA
                                                                     1800 TGAAGGCGGCCAAAGTGCTGCGGGAGCAGCTATTGACCAGCTACTTGATTTCCATCCGGC
                                                                                                                                                                   1860 TGTTGAAGAAGCTCGCGAAATGGCACAACGTGTGAATCAGCCCCTCCCCGGTCTGGCTTGC
                                                                                                                                                                                                                      42888 CTATCCGGCACTGCTGGAACAGGCTAAAAATAAGGGCGAAACCATCTATGAGGCGCTGAA
                                                                                                                                                                                                                                                                    TGATCGAATCCTCGAAAAAAACGGCGCAACCATCAGATGCTGTCGCCCTGGCGAAAGGGCT
                                                                                                                                                                                                                                                                                                                                                                        ACACGTGGTGCCGGAATTTCTCGGAAATCGCGCCCCCTTCGCAGATCCTCATGCCAGAGC
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CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre
BC Cancer Agency, Vancouver, BC, Canada
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Contact: MGC help desk
Emall: cgapbs.r@mail.nih.gov
Tissue Procurement: ArCc/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini
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BC014947.1 GI:15928958
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BC014947
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COMMENT
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/traislation-"MUDHRAVSQVNRINETKHSVLQVGGVMSVEMOAPKLLWLKEN
LREIGMDKAGHEFDLEDELSKKATGYTARSLCSLVCKWTYSAEKGWDDSFWKMIGLED
VRADNYSKIGNOVLPPGASLGNGLTPENARDLGLLEGIAVAASLIDAHAGGLGVIGAD
VRGHGLICEGOPYTSRLAVICGTSSGHMGISKOPIEVPGWGPYFSAMVDGFWLNEG
GSVTGKLIDHMVQGHAAFPELQVKATARCQSIYAYLNSHLDIKKAQPVGFLTVDLHV
WPDFHGNRSPLADLTLKGMYTGLKLSODLDDLAILYLATVOAIALGTRFIIEAMEAAG
HSISTLFLGGCLSKNPLFVQMHADITGMPVVLSQEVESVLVGAAVLGACASGDFASVQ
422 c 520 g 495 t
422 c 550 g
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                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 34 Row: I Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 10433590.
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Less, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jaff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1059 GGCAGACGTTTGTGCACAAAGTGTGGCAGGCATCGGTTTTGATGCCACCTGTTCTGGT 1118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGCTATCCCATGCCACAGAAAAATCACGACTACGCGGCGCGCGGGAAGCCGCGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 CCTGTTGGCTTTTGCAGACCAGCCAATTAAGAATTGGGAGCCCCAGTTCAACCACCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 TGTTTTGGATAAGCAGTTTCACCCATTACCAGTCAACCAGGAAGGGGATTCCCATCGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Unknown (protein for MGC:22958)"
/protein_id="AAH14947.1"
/db_xref="GI:15928959"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Skin, melanotic melanoma,
/clone_lib="NnH_WGC_49"
/lab_host="PHIOB-R"
/note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 302.4; DB 9;
Pred. No. 1e-76;
0; Mismatches 716;
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo saplens"
/db_xref="taxon:9606"
/clone="MGC:22958 IMAGE:4871664"
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52.18;
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827; Conservative
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			; Ve ni;	SF, H,	J., and tics		1.de	B 6;	ATTI CTGC) - - - -	ATTC ACAA	GATC	GAAC	GAGC - AACA	GAAA	CGTC	GCGC	GATC
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1708	1991 bp WO0121836		Chordata; Craniata; V. Primates; Catarrhini;	Rus G. F. Jone	Ams Ind 1	Figures, Inc. (US) Location/Qualifiers 1. 1991 /organism="Homo sapiens"	 6 0 _	Score 300.8; Pred. No. 3e- ; Mismatches	GGATCAGGCAGTGTCCG 	CGA(17.17. 17.17.07.07.07.07.07.07.07.07.07.07.07.07.07	GCAT - GACT	CTG	CCG	AAAT TGAT	.T:	CAGG	AAA
	199 WO01		rdat mate	.E.,	A.M. .K., .K., 229-N	fier fier	on:95 ID N 534 g	Яe	AGTG -	AATCA AATTA	9000 0000	GCAC	TTGC	GCCP GCAG	GGT# - GGGG	AGAGAT AGAGAT	GCTA 	CATO
 GAAG	ent	537641		ln, S Duf n, J.	rry, er,T osti	Location/Qualifiers 1. 1991 //Organism="Homo sap	raxo yte 5	0	AGGC AGGC	AAAA 	GCAG 	TGTG AATT	17CC.	TGTGGATGGATCACCGC(TGTGGCTGGACCATCGA(CGGT 	TGCCA TGAGA	GCGG GAAG	GGCA
rccr	Patent	2153	20a; ria;	inco R., Ilma	dreb iagn 836-	on/0 91 ism=	"Inc 7 c	7.6%; ilarity 52.0%; Conservative	SATC SAAC	CAGA ACCA	ATCTGG 	AAAG ACCA	STGA TCA	ATCA ACCA	ACGT ACGT	ATAT ACTT	CCTG CGTG	SGCT
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ATAC	7495 ence	7495	n. sap ryot alia	son, cher up, N	P.E.	ם פ	468	Similarity 6; Conser	TGT1 TGT0	ATCC GGCT	CAGO	CGT	GGAT	TGTO	GGTC	GCTC	CGAT	TAA
	AX427495 Sequence	AX427 AX427	numan. Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria;	L Hodg Brat Chal	Fanzer, S.K., RoseDerry, A.M., Wirght, K.J., Chen, W., Liu, T., Yap, P.E., Stockdreher, T.K., Amshey, S. and Fong, W.T. Molecules for diagnostics and therapeutics Patent, WO 0121836-A 5 29-WAR-2001;	TIICA		ch 1 Sim 826;	TATTGGTGTTGATGTGGGATCAGGCAGTGTCCGCGGCGGATTTTTGATCTCAACGGATCT	TCTGCTATCCCATGCACAGAAAAATCACGACTACGCGGCGCGGCGGAAGCCGCGTGGA 	ACAGTCCAGCCAGGAGATCTGGCAGGCGGTCTGTTCATGTATTCGTAATGCGCTCACTCT	GGCAGACGTTTGTGCACAAAGTGTGGCAGCATCGGTTTTGATGCCACCTGTTCTCTGGT 	GGTACTGGATAAAAAGGGTGATCCATTGCCTGTCAGCCGGAAGGAGATGCAAAAGAAAA	TATCATTGTGGGATGGATCACCGCGCCACCGAACAAGCAGAGCGAATCAATGCCACTCA	CCATCCGGTGCTGAACTACGTCGGTGGTAAAATTTCGCCTGAAATGGAAAGACCGAAAAT 	TCTCTGGCTGAAAGAAATATGCCAGAGATCTACGAACGTGCCGGACAATTTTTCGA 	TCTGGCCGATTTCTGACCTGGGGGCTACCGGTGATTTAGCGCGTTCAGTATGCACTGT	TACCTGTAAATGGACGTGGCTGGCACATGAAAATCGCTGGGATCCAGATTATTTCCGCAC
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1681	7495 3 VITI	SSIO	ORGANISM	PHOR	TITLE JOURNAL	JRES	COU	Query Match Best Local 9 Matches 820	879	939	347	1059	1119	1179 521	1239 581	1299	1356 701	1416
qq	RESULT 12 AX427495 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE	AUTHORS	TIL	FEATURES sou	BASE COUNT ORIGIN	Mage	oy Ob	Oy Dp	Qy Db	Qy Db	Qy Dp	QY Db	Qy Db	Oy Db	. qa	οy
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356 TCTGGCCGATTTCTGACCTGGCGGGCTACCGGTGATTTAGCGCGTTCAGTATGCACTGT 1415		CATIGGCCTIGCAGAGITAGCGGAIGAAGAITITATICGCAITGGICAICAIATITITI 1535 	TCCCGGAACACCTTGTGGAAATGGTTTAACAGCACAGCGCGGCGGGGGGGG	CCCCGGCACACTGTCGCTGTAGGGTTAATTGATGCTCACGCTGGTGGCATCGGTACGGT 1655 	TGGCGTAGAAGGTGGAGCGC	CGCGTATGTTTTCGGCACTTCTTCATGCACCATGGCATCTACCACTTCTCCCTGGTTTGT 1745	1746 ACCGGGTGTCTGGGGGCCGTATTACAGTGCGATGGTTCCAGGTCTGTGGTTAGTTGAAGG 1805 	CGGGCAAAGTGCTGCGGGGGCAGCTATTGACCAGCTACTTGATTTCCATCCGGCTGTTGA 1865 	1866 AGAAGCTCGCGAAATGGCACAACGTGTGAATCAGCCCCTCCCCGTCTGGCTTGCTGATCG 1925 	1926 AATCCTCGAAAAACGGCGCAACCATCAGATGCTGTCGCCCTGGCGAAAGGGCTACACGT 1985 	GGTGCCGGAATTTCTCGGAAATCGCGCCCCTTCGCAGATCCTCATGCCAGAGCGGTAAT 2045 	TTGTGGCCTGGGTATGGAGGAGATCTGGATAATTTACTCGCCTÄGTATTCGCTGGATT 2105 	ATGCGGAATTGGTTATGGTCTGCGCCAAATTCTCGACGCTCAAACAGCGCAGGGGTAGT 2165 	GAGTAAAAATATCGTTATTAGCGGCGGTGCCGGCCAGCATCCACTGGTACGACAAATTCT 2225 	GGCAGATACTGCGGTATTCGGGTCATTACCACGCAATGCTGCGAACCGGTTTTATTAGG 2285 	CTCGGCCATICITGGTGCTGTCGCCGGAAATATTGCACCTTCTGTTGGCGAAGCGATGCA 2345 	ACAAȚTCACCCATGTGGATAATATTATCGCAAGAACGĆTATCAATCTCTTCATCA 2405 	TCGTCGATATGAGGCCTATAAGCAGTTG 2433
Qy 1356 TCTC Db 607 TCTC		Oy 1476 CAT	Oy 1536 TCCC Db 784 TCCT	0y 1596 CCCC Db 844 CCC	Qy 1656 TGG Db 904 TGG	Oy 1686 CGC 1 Db 964 GGC	Oy 1746 ACCO	Qy 1806 CGGG 1 1 Db 1084 TGG	Qy 1866 AGA Db 1144 AGA	Qy 1926 AATO Db 1201 TCAO	Qy 1986 GGTC Db 1261 TTGC	Qy 2046 TTG Db 1321 CAC	Oy 2106 ATG	Oy 2166 GAG' Db 1441 AATC	Oy 2226 GGCJ 	Qy 2286 CTC(Db 1561 TGC	Qy 2346 ACA Db 1621 AAAA	Qy 2406 TCG3

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                                      CATTGGCCTTGCAGAGTTAGCGGATGAAGATTTTATTCGCATTGGTCATATTGTTTC
                                                              GATTGGTTTGGAAGACTTTGTTGCAGATAATTACAGCAAAATAGGAAACCAAGTGCTACC
                                                                                         1536 TCCCGGAACACCTTGTGGAAATGGTTTAACAGCACAAGCCGCGGCAGAGATGGGATTACT
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/db_xref="taxon:9606"
/clone="ASTR02005081"
/cell_tp="namal astrocytes (NHA5732)"
/clone_llb="ASTR02"
/note="cloning vector: pME185FL3-primary culture, normal
                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagai, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irle, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Ison Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H. Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Mirawa, K., Kanehori, K., Takahashi-Fuji, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Naga and Isogai, T.
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Catarrhini; Hominidae;
                                  mRNA linear
clone ASTRO2005081,
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Homo sapiens normal astrocytes (NHA5732) cDNA
clone_lib:ASTRO2 clone:ASTRO2005081.
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tive 0; Mismatches 664;
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Homo sapiens CDNA FLJ33249 fis,
to L-RIBULOKINASE (EC 2.7.1.16).
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Mammalla; Eutheria; Primates;
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1574 TGCGGACATTACTGGCATGCCTGTGGGCCTGTCGCAAGAGGTGGAGTCCGTTCTTGTGGG 1633

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                                                                                                1299 TCTCTGGCTGAAAGAAATATGCCAGAGATCTAC---GAACGTGCCGGACAATTTTTCGA 1355
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1239 CCATCCGGTGCTGAACTACGTCGGTGGTAAAATTTCGCCTGAAATGGAAACACCGAAAAT
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/product="Similar to RIKEN cDNA 2310009E04 gene"
/protein_id="AaH31708.1"
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/db_xref="G1:21618804"
/translation="MMSGRDGEPSRYVGIDVGTGSVRAALVDQRGLLLAFAEQPIKK
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DNYSKIGNLVLLPGAALGTGLTPEAARELGLPSGIAVASLIDAHAGGLGVIGADVR
HGLTCEGQPVTSRLAVICGTSSCHMGISKDPVFVPGWMGPYYSAMVPGFWLNEGGGSV
TGKLLDHWVQGHPAFPELQAKATARNLQKHHGIHGDTFGIAKVELEVTSSKAF"
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 1842)
Strausberg,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 30 Row: o Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M. Richards, S., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmo.edu
                                                                                                                                                                                       BC031708 1842 bp mRNA linear ROD 07-
Mus musculus, Similar to RIKEN cDNA 2310009E04 gene, clone
MGC:25851 IMAGE:4194716, mRNA, complete cds.
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CTCGGCCATTCTTGGTGCTGTCGCCGGAAATATTGCACCTTCTGT
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/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
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/organism="Mus musculus"
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Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Chen, Y., Woo, L., Kitajima, J.P., Okura, V.K., Almeida Jr., N.F., Chen, Y., Bovee Sr., D., Chapman, P., Clendenning, J., Deatherage, G., Gillet, W., Grant, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M., McClelland, E., Palmieri, A., Raymond, C., Rouse, G., Saenphimmachak, C., Wu, Z., Gordon, D., Elsen, J.A., Paulsen, I., Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M., Kraspan, W., Perry, M., Gordon-Kamm, B., Liao, L., Kim, S., Hendrick, C., Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Chen, Y., Woo, L., Kitajima, J.P., Okura, V.R., Almeida Jr., N.F., Chen, Y., Woo, L., Kitajima, J.P., Okura, V.R., Almeida Jr., N.F., Shou, Y., Bovee Sr., D., Chapman, P., Clendenning, J., Deatherage, G., Gillet, W., Grant, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M., MCCIelland, E., Palmieri, A., Raymond, C., Rouse, G., Rouse, G., Saenphimmachak, C., Wu, Z., Gordon, D., Eisen, J.A., Paulsen, I., Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M., Krespan, W., Perry, M., Gordon-Kamm, B., Liao, L., Kim, S., Hendrick, C., Zhao, Z., Dolan, M., Tingey, S. V., Tomb, J., Gordon, M.P., Olson, M.V.
                      DNA linear BCT 20-DEC-2001
linear chromosome, section 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-SEP-2001) Department of Microbiology, University of Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA 98195-7242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer" /codon_start=1
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Agrobacterium tumefaciens str. C58 (U. Washington)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The genome of the natural genetic engineer Agrobacterium tumefaciens C58
Science 294 (5550), 2317-2323 (2001)
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11164 bp ...
                                             Agrobacterium tumefaciens str. C of 187 of the complete sequence. AE009374 AE008689
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                                             DEFINITION
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AUTHORS
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AUTHORS
                                                                                                      ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                992 GCGTGGAACAGTCCAGCCAGGAGATCTGGCAGGCGGTCTGTTCATGTATTCGTAATGCGC 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2429 CCGGCCGGCTGCTCGCGCGCTCCATTCATCCTCATGCAGCGGCCGCGTGAAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 11164;
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Matches 714; Conservative
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BREPDITWARGSAORSNCTGTRAKURTAGGHRAFAGLDDLKERAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIAGTSSCLVAMSTQPMPGRSLWGPYWQAVLPGHWLVEGGQSATGALLDHIVRMHAAG
GEPDTALHARIVARVTELRELEGEAFADRLHVLPDFHGNRSPLADPHAVGVVSGLTLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLSLSPWTVGRFLRSLGYROFSDIRADLRHAEETVGADQPVTAEGGERHSNPFSQLLS
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GPESVDLCLAMPQSQNGGOGLLQLVSLLEFTLCALSAGADDAGKARYKNLAALKRSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MNGDAFARPCKRANHDLTVETSFPGHVLHRTGMRIIVDGLLYFRAIFYSREIPFAV"
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YRRFLAMYRHRQELESL"
                                                                                                                                                                                                                                                                                                                                                                                     PRQCIVIEDSPAGIAAAKAAGMGVFAFTGGSHARFPAFREKIAGLGADAVFDAMPDLV
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complement(4041...4874)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product "transcriptional regulator, RpiR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glimmer"
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3370 3475 1:111 1112 CTCTGGTGGTACTGGATAAAAACGGTGATCCATTGCCTGTCAGCCCGGAAGGAGGAGCAA 1171 1172 AGCAAAATATCATTGTGTGGATGGATCACCGCGCCCACCGAACAAGCAGGGGGGAATCAATG 1231 2729 CCTCGGGCCATCGGGGGGGGTTCGCCGGCAACAGCGTCTCGCCGGAAATGCAGATGC 2788 1292 CGAAAATTCTCTGGCTGAAAGAAAATATGCCAGAGATCTACGAACGTGCCGGACAATTT 1351 2848 1411 2849 TCGATCTCGCGGGATTTCCTGACCTGGAGGCGACCGGCTCGGCACGCCTCCAATTGCA 2908 1412 CIGTTACCTGTAAATGGACGTGGCACATGAAAATCGCTGGGATCCAGATTATTTCC 1471 1472 GCACCATTGGCCTTGCAGAGTTAGCGGATGAAGATTTTATTCGCATTGGTCATCATATTG 1531 1652 CGGTTG-----GCGTAGAAGGTGGAGCGCTGAACAATCTCGCGTATGTTTTCGGCACTT 1705 1706 CTTCATGCACCATGGCATCTACCACTTCTCCCTCGTTTGTACCGGGGTGTCTGGGGGGCCGT 1765 3262 1766 ATTACAGTGCCATGGTTCCAGGTCTGTGGTTAGTTGAAGGCGGGCAAAGTGCTGCGGGAG 1825 1826 CAGCTATTGACCAGCTACTTGATTTCCATCCGGCTGTTGAAGAAGCTCGCGAAATGGCAC 1885 1886 AACGTGTGAATCAGCCCCTCCCCGTCTGGCTTGCTGATCGAA,CCTCGAAAAACGGCGC 1945 1946 AACCATCAGATGCTGTCGCCCTGGCGAAAGGGCTACACGTGGTGCCGGAATTTCTCGGAA 2005 2006 ATCGCCCCCTTCGCAGATCCTCATGCCAGAGCGGTAATTTGFGGCCTGGGTATGGAGC 2065 3476 ACCGTTCGCCGCTTCCCGATCCGCTCGCGCTCGCGCTCAGCGGCTGACGCTCGATA 3535 GAGATCTGGATAATTTACTCGCCTTGTATATCGCTGGATTATGCGGAATTGGTTATGGTC 2125 1232 CCACTCACCATCCGGTGCTGAACTACGTCGGTGGTAAAATTTCGCCTGAAATGGAAACAC 1291 1532 TITCTCCCGGAACACCTTGTGGAAATGGTTTAACAGCACAAGCCGGGGGGAGATGGGAT 1591 1592 TACTCCCCGGCACACCTGTCGCTGTAGGGTTAATTGATGCTCACGCTGGTGGCATCGGTA 1651 3143 CTCTGGGTGGATGCCTTGCCGAGGATGTCGGTAAACATGTCGCGCTGATCGCCGGCACGT 3202 3029 TGCCGGGCGCCCATCGG-----CCCGCTTTCGCCCCGAGGCCGCCGCAGAACTTGGTC 1052 TCACTCTGGCAGACGTTTGTGCACAAAGTGTGGCAGGCATCGGTTTTGATGCCACCTGTT 2609 CGCTGGTCATCCGCGATGAGCGGGGGGGGCGCTTTCGGTTTCCACGACCGATGACGACC 3203 CGAGTTGCCTTGTCGCCATGTCCACGCAGATGCCCGGCGCACCTTGTGGGGACCCT 1352 TCGATCTGGCCGATTTTCTGACCTGGCGGGCTACCGGTGATTTAGCGCGTTCAGTATGCA 3430 g g a g ò g qq g qq Ω ò g ò g ò g ò ò g õ ò ò õ ò ö g ò Dp ò g ò g ò ò g ò

2245 3536 CCTCCTTCGACAGTCTCTGCCGTCTTTATTGGCGCACCGCGATCGCGATCGCGCTCGGCG 3595 2186 GCGGCGGTGCCGGGCAGCATCCACTGGTACGACAAATTCTGGCAGATACCTGCGGTATTC CGGTCATTACCACGCAATGCTGCGAACCGGTTTTATTAGGCTCGGCCATTCTTGGTGCTG 2126 TGCGCCAAATTCTCGACGCTCAAACAGCGCAGGGAGTAGTGAGTAAAAATATCGTTATTA 2306 TCGCCGG 2312 3776 cGccccc 3782 2246 음 ò qq ò QQ ò q ò qq

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Listeria monocytog

Human ORFX ORF2764

Human prostate exp Plasmid pAN296 for Novel pantothenate

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Positive selection system; metabolise; arabitol; ribitol; mannitol; transgenic cell; marker gene; ribitol dehydrogenase; ribitol kinase; ribitol transporter; rtl operon; ds.
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XX A (UYGE-) UNIV GEORGIA RES FOUND INC.

XX PRIS. 2001-565596/63.

PPSDB: AAE09779, AAE09780, AAE09781.

The present invention relates to a positive selection marker compounds e.g., arabitol, ribitol which confer selective advantage on transformed CC involves conferring to transferred cells the lability to metabolise arabitol, ribitol and/or manitol. The positive selection method is conferring to transferred cells the lability to metabolise arabitol, ribitol and/or manitol. The positive selection method is conferred in positive selection method, the presence of the gene of interest in the genetically transferred cells from a population of cells confered with transformed cells may be identified by simple visual means without the consolidation of the transformed cells may be identified by simple visual means without the consolidation of the relasse of a marker gene. This cechnique also avoids the release of antibiotics or other dangerous cells in the density of the relasse of antibiotics or other dangerous cells and ribitol transporter.

XX Sequence 3971 BP: 919 A: 930 C: 1020 G: 1102 T: 0 other:
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Sequence 3971 BP; 919 A; 930 C; 1020 G; 1102 T; 0 other;

Query Match

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3971; Conservative 0; Mismatches 0; Indels 0; Gaps

; 0 240 240 300 420 480 480 540 9 9 CAGAGACTATAAATTCGCCCTGGTAAAAGGATTATATGATGAATCACTCTGTGCCCTCTA TGAATACTCCCCTTAATGGCAAAGTTGCAGCTATCACTGGCGCTGCGTCAGGTATTGGCC GTGCAGTCCTGCCGCATATGATTGCGCAGAGGTCGGGCGATATAATTTTACCAGTTCCA GCCTGGATATTTTCATGCCAATGCAGGCGCTTATATTGCGCGGCCCAGTGGCTGAAGGTG ATCCAGATGTCTGGGATCGTGTTAAATCTGAATATAAATGCGGCGTTTCGCTGTGTCC 61 121 121 181 61 181 241 241 301 301 361 421 481 361 421 g ò ò g ô 8 õ a ò Q ð g ò g à q ò

1020 1140 1140 540 99 720 780 780 840 840 099 720 900 900 960 960 GFGCAGTCCTGCCGCATATGATTGCGCAGAGGTCGGCGGATATAAATTTTACCAGTTCCA TGCTGCCAGGACCAGTAGTCACTGCCTGCTTGATGACTGGCCAAAAAGCCAAAATGGAAG ATCTGTAAGGGCGCAATCATGACAATAACCAAAACCGTTATTGGTGTTGATGTGGGATCA ATCTGTAAGGGGGGCAATCATGACAATAACCAAAACCGTTATTGGTGTTGATGTGGGATCA GGCAGTGTCCGCGCGGGATTTTTGATCTCAACGGATCTCTGCTATCCCATGCCACAGAA AAAATCACGACTACGCGCGCGCGCGCGCGCGCGTGGAACAGTCCAGGAGATCTGG CAGGCGGTCTGTTCATGTATTCGTAATGCGCTCACTCTGGCAGACGTTTGTGCACAAAGT GTGGCAGGCATCGGTTTTGATGCCACCTGTTCTCTGGTGGTACTGGATAAAAACGGTGAT CGCGCCACCGAACAAGCAGAGCGAATCAATGCCACTCACCATCCGGTGCTGAACTACGTC CCAGAGATCTACGAACGTGCCGGACAATTTTTCGATCTGGCCGATTTTCTGACCTGGCGG CATGAAAATCGCTGGGATCCAGATTATTTCCGCACCATTGGCCTTGCAGAGTTAGCGGAT GAAGATTTTATTCGCATTGGTCATCATATTGTTTCTCCCGGAACACCCTTGTGGAAATGGT TTAACAGCACAAGCCGCGGCAGAGATGGGATTACTCCCCGGCACACCTGTCGCTGTAGGG 781 841 1021 1081 1081 1141 1141 1201 1201 1261 1261 1321 1321 1381 1381 1441 1441 1501 541 601 661 721 721 781 841 901 901 961 1021 1501 1561 481 109 661 961 à g ò g δ 셤 ò q ò Db ò a ò g ò Ор ò q ò Q Οy qq δ QΩ ò Вp ò QΩ à q ò a ò q ò m

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51 TTAACAGCACAAGCGGGGAGAGATGGGATTACTCCCGGCACACCTGTCGCTGTAGGG 1620	621 TTAATTGATGCTCACGCTGGTGGCATCGGTACGGTTGGCGTAGAAGGTGGAGCTGAAAC 1680 -	681 AATCTCGCGTATGTTTCGGCACTTCTTCATGCACCATGGCATCTACCACTTCTCCCTCG 1740 	1 TTTGTACCGGGTGTCTGGGGGCCGTATTACAGTGCGATGGTTCCAGGTCTGTGGTTAGTT 1800	11 GAAGGCGGCAAAGTGCTGCGGGAGCAGCTATTGACCAGCTACTTGATTTCCATCCGGCT 1860 	861 GTTGAAGAAGCTCGCGAAATGGCACAACGTGTGAATCAGCCCCTCCCCGTCTGGCTTGCT 1920 		11 CACGIGGIGCCGGAAITICICGGAAAICGCGCCCCTICGCAGAICCICAIGCCAGAGCG 2040	11 GTAATTTGTGGCCTGGGTATGGAGCGAGATCTGGATAATTTACTCGCCTTGTATATCGCT 2100 	11 GGATTATGCGGAATTGGTTATGGTCTGCGCCAAATTCTCGACGCTCAAACAGCGCAGGGA 2160 	 SI GTAGTGAGTAAAAATATCGTTATTAGCGGCGGGGGGCGGCCAGCATCCACTGGTACGACAA 2220 SI GTAGTGAGTAAAAAATATCGTTATTAGCGGCGGGCGGCCAGCATCCACTGGTACGACAA 2220 	11 ATTCTGGCAGATACCTGCGGTATTCCGGTCATTACCACGCAATGCTGCGAACCGGTTTTA 2280	31 TTAGGCTCGGCCATTCTTGGTGCTGTCGCCGGAAATATTGCACCTTCTGTTGGCGAAGCG 2340 	11 ATGCAACAATTCACCCATGTGGATAAATATTATTATCCGCAAGAACGCTATCAATCTCTT 2400		 TAATTAACCAGCCGCTGACGCTGTTTTCAGGCAATCACTAATÄACGACTCCCGGTA 2520 TAATTAACCAGCCGCTGACGCTGTTTTCAGGCAATCACTAATAACGACTCACTC	11 ATATCCCGGAGTGCATTCATCTGCACCCTAAAAACGAGGTTTATATGTCCAGAAATAATA 2580 	31 AACAGTGGGTTTGCCACTGCATCTGATATGGGGATATATCGCCATCGCAGTATTTA 2640 	1 TGACTGGTGATGGTTTCGAACTCGCATTCTTATCGCACTATATAAATCGTTAGGCTTCA 2700
b 156			y 1741 o 1741	y 1801 b 1801	1	y 1921 5 1921	y 1981 b 1981	y 2041 b 2041	y 2101 b 2101	y 2161 b 2161	y 2221 b 2221	y 2281 b 2281	y 2341 b 2341	y 2401. b 2401	y 2461 b 2461	y 2521 b 2521	y 2581 b 2581	y 2641
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open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                  3960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding a Staphylbcoccus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                               nucleic acid sequence SEQ ID NO:183
 TTGAGCAGCCAGGATTCAGTTCTGCGCCAGTGACTGAGAAGGCATTGAATATCTCCTGAA
             AAACGAAACGCATCAGGCACTCATCCTCCCTCATGGGAGGAGGATGATTTCACATCAGG
                                                                        Sequence 1401 BP; 242 A; 329 C; 418 G; 411 T; 1 lother;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID 183; 267pp; English.
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160 TTCGGTTTACCCATATCTCTGATTTGGGGGTTTGTGGCCCATTGCCGTGTTCATGACCGGG 219
                                                                     220 GATGGAATTGAACTAGGGTTTCTCTCCCGATATGTAGTTGATCTGGGTTTCTCCCCTACT
                                                                                                                                                                      280 CAGGCAACTCTTTTTACGGTCTATGGTTTTTTGCAGCCATTTCAAGTTGGGGTTCC
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0; Mismatches 555; Indels

7.8%; Score 311; DB 24; 4.1%; Pred. No. 5.5e-88;

54.18;

657; Conservative

Matches

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Similarity

Query Match Local

Length 1401;

2589 TIGGGTTTGCCACTGCATCTGATATGGGGATATATCGCCATCGCAGTATTTATGACTGGT 2648

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The invention relates human kinases (PKIN) and their corresponding nucleic acid sequences. PKIN and its DNA are useful for diagnosing, treating and preventing cancer, an immune system disorder (e.g., acquired immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma, atherosclerosis, multiple sclerosis, psoriasis), disorders
                 1300 TGGATCTACGCAGGCTCTACGTGCCGGTGCGGTTTTGACCTTCTTCATTCCTGTCCCT 1359
                                                                                                                                                                                                                                                                                        Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis; acquired immune defictency syndrome; AIDS: Addison's disease; allergy; asthmine multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis; development; hepatitis; cardiovascular; hypertension; drug screening; myocardial infarction; Goodpasture's syndrome; lipid disorder; growth; fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic; hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hIV; neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic; hyperlipidaemia; enzyme; gene; ss.
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umar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB;
uu Y, Yue H, Burford N, Bandman O, Tribouley CM;
pon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human kinase polypeptide, for diagnosing, preventing and treat cancer, immune system disorders, growth and development disorders, cardiovascular disorders and lipid disorders
/product= "Human kinase (PKIN)-11"
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Lal PG, Recipon SA, Lu DAM, Borowsky ML,
Thangavelu K, Khan FA, Ison CH;
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2000US-247672P.
2000US-249565P.
2000US-252730P.
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affecting growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis), cardiovascular disorder (e.g., hypertension, myocardial infarction, Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver, Gaucher's disease, Namann-Pick's disease, hypercholesterolaemia, hyperlipidaemia, obesity), and for assessing the effects of exogenous compounds. Anti-PRIN antibody is useful in a diagnostic test for a condition or a disease associated with the expression of PKIN in a biological sample. A composition comprising PKIN or an agonist or antagonist of PKIN is useful for treating a disease or condition associated with decreased or increased expression of functional PKIN. It is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN DNA is useful for creating knockin humanised animals or transgenic animals to model human diseases, and in somatic or germline gene therapy. The present sequence is human and the second of the control of the proteome of a tissue or cell type.
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                                                                                                                                                                                                                                                                                                                                                         24; Length 1876;
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Pred. No. 3.8e-85;
0; Mismatches 716; Indels
                                                                                                                                                                                                                                                                                                                  Sequence 1876 BP; 468 A; 400 C; 519 G; 489 T; 0 other;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemctactic/chemckinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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Zhang J;
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Yang Y,
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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                                                        2000US-0488725.
2000US-0552317.
2000US-0598042.
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Best Local Similarity 52.1%;
Matches 827; Conservative
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Wang J, V
Zhao QA,
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                                                                                                                       AATCAGTACTCTTTTCCTATGTGGAGGCCTCAGCAAGAATCCCCTTTTTGTGCAAATGCA 1641
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                                                                                                                                                                                                                                                                                                                Human diagnostic and therapeutic molecule; dithp; gene therapy; thalassemia; cardiovascular disorder; cell proliferative disorder; cancer; neurodegenerative disorder; autolmmune disorder; enzyme; infectious disorder; inflammatory disorder; developmental disorder; Incyte ID number 05377811dec; ss.
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BH, Shah P, Chalup MS;
LB, Panzer SR;
                     GGCAGATACCTGCGGTATTCCGGTCATTACCACGCAATGCTGCGAACCGGTTTTATTAGG
                                                                                                                                                                                                                                                                                            Human diagnostic and therapeutic (dithp) cDNA sequence #5
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                                                                                                                                                                 TCGTCGATATGAGGCCTATAAGCAGTTG 2433
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1, Wright RJ, Chen
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Bratcher SR, Dufour GE,
Hillman JL, Jones AL, Yu
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Novel diagnostic and therapeutic polynucleotides, used in disease diagnosis and for gene therapy of conditions such as cancer and thalassemia.
                         Claim 1; Page 253-254; 299pp; English.
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The present sequence for human diagnostic and therapeutic (dithp) cDNA sequence #5 is 1 of 71 (AAS03012-AAS03082) novel sequences described in the invention. The present sequence (Incyte ID No: 05377811dec) corcodes an enzyme molecule. The dithp polynicicotides may be used to diagnose a condition disease or disorder associated with human nucleic acids. Dithp polynucleotides may used to generate hybridisation probes for use in chromosomal mapping. Polypeptides (DITHP) encoded by disorders such as severe combined immunodeficiency syndrome (SCLD), cystic fibrosis, thalassemia, haemophilia resulting from Factor VIII cyracidesness, cardiovascular disorders, e.g familial hypercholesterolaemia (FH), cell proliferative disorders e.g. cancers, neurodegenerative disorders, autoimmune/inflammatory disorders. infectious disorders and developmental disorders. The antibodies can be used to analyse protein expression levels.

Sequence 1991 BP; 468 A; 467 C; 534 G; 516 T; 6 other;

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999 ACAGICCAGCCAGGAGAICIGGCAGGCGGTCTGTICAIGTATTCGTAAIGCGCTCACICT 1058 1059 GGCAGACGTTTGTGCACAAAGTGTGGCAGGCATCGGTTTTGATGCCACCTGTTCTCTGGT 1118 1179 TATCATTGTGTGGATGGATCACCGCGCCACCGAACAAGCAGAGCGAATCAATGCCACTCA 1238 1475 1298 1355 1415 640 400 460 520 700 760 346 879 TATTGGTGTTTGATGTGGGATCAGGCAGTGTCCGCGGCGCGGATTTTTGATCTCAACGGATC 938 227 TGTGGGTGTGGACGTTGGAACAGGCAGTGTCCGTGCAGCTCTGGTGGACCAGAGTGGGGT 286 Gaps 939 TCTGCTATCCCATGCCACAGAAAAATCACGACTACGCGGGGCAGCGGAAGCCGCGTGGA 287 ccrerregerrriccagaccagecaarraagaarregeagecccagrecaccaccarda CCATCCGGTGCTGAACTACGTCGGTGGTAAAATTTCGCCTGAAATGGAAACACGGAAAAT TCTCTGGCTGAAAGAAAATATGCCAGAGAT----CTACGAACGTGCCGGACAATTTTTCGA 1356 TCTGGCCGATTTTCTGACCTGCCGGCTACCGGTGATTTAGCGCGTTCAGTATGCACTGT TACCTGTAAATGGACGTGGCTGGCACATGAAAATCGCTGGGATCCAGATTATTCCGCAC GGTGTGTAAGTGGACATATTCAGCA---GAGAAAGGCTGGGACGACAGTTTCTGGAAAAT CATTGGCCTTGCAGAGTTAGCGGATGAAGATTTTATTCGCATTGGTCATCATATTGTTTC 401 ACAAGGGATTGATTTAAACCAAATTCGAGGACTTGGGTTTGATGCCACGTGTTCTCTGGT Score 300.8; DB 22; Length 1991; Pred. No. 1.3e-84; 0; Mismatches 717; Indels 45; 7.68; 52.0%; Matches 826; Conservative Best Local Similarity Query Match 1299 1416 1119 701 1476 g g a 셤 g ð ô ò q å ò qq ò ò ò පි ò g ò g ŏ

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ABL26431 standard; DNA; 2602

ABL26431

(first entry)

26-MAR-2002 ABL26431;

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                                                                            TGGGGCAGATGTGAGAGGGCACGGCCTCATCTGTGAGGGGCAGCCAGTGACGTCACGGCT
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TCCCGGAACACCTTGTGGAAATGGTTTAACAGCACAAGCCGCGGCAGAGATGGGATTACT
              CCCCGGCACACCTGTCGCTGTAGGGTTAATTGATGCTCACGCTGGTGGCATCGGTACGGT
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                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                     Drosophila; developmental biology; cell signalling; insecticide;
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              NO 30766.
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Pred. No. 5.3e-56;
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(ull-length cDNas defined in the specification, Where a primer set
comptises: (a) an oligo-dT primer and an oligonuclectide comptimentary
to the complementary strand of a polynuclectide which comprises one of
the 5602 nuclectide comprises at least 15 nuclectides; or (b) a combination
of an oligonuclectide comprising a sequence complementary to the
complementary strand of a polynuclectide which comprises a 5'-end
sequence and an oligonuclectide comprising a sequence complementary to the
complementary strand of a polynuclectide which comprises a 5'-end
sequence and an oligonuclectide comprising a sequence complementary to the
polynuclectide which comprises a 1'-end sequence, where the
oligonuclectide which comprises a 1'-end sequence, where the
oligonuclectide which comprises as 1'-end sequence, the pagenerical and these combination of
the 5'-end sequence, 3'-end sequence; selected from those defined in
the specification. The primers are useful for synthesising polynuclectides,
particularly full-length cDNAs. The primers are also useful for the
particularly full-length cDNAs. The primers are also useful for the
cubnas easily without any specialised methods. AAH13628 and
AAH13633 to AAH13629 to AAH13632
ceptresent human amino acid sequences; and AAH13629 to AAH13632
ceptresent pullopurclectides, all of which are used in the exemplification
                                                                                                                                                                                                      Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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4.6%; Score 183; DB 22; Length 1947;
Best Local Similarity 56.3%; Pred. No. 6.2e-47; Handle Se; Conservative O; Mismatches 295; Indels 36;
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A, Nagai K, Otsuki T;
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Sugiyama T, Wakamatsu A,
                                                                                                                                                                     Human cDNA sequence SEQ ID NO:13883
                                                                 AAH15580 standard; cDNA; 1947 BP.
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0241899.
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AGCGAATCAATGCCACTCACCATCCGGTGCTGAACTACGTCGGTGGTAAAATTTCGCCTG
                GTGCCGGACAATTTTCGATCTGGCCGATTTTCTGACCTGGCGGGCTACCGGTGATTTAG
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pharmaceutical; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 30763; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                         2553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5019 BP; 1402 A; 1055 C; 1191 G; 1371 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection
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                                                                                                   TGGTTTAACAGCACAAGCCGCGGCAGAGATGGGATTACTCCCCGGCACACCTGTCGCTGT
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                                                                                     AGGACTCACGGCCAAGGCTGCTGGGGAACTGGGCTTATCCGCCGGCACTGTGGTGAGCAC
                                                                                                                                             ACAGAATAACTTCGAGAAATTGGGCAGTGATGTCCAGCCGCCTGGCCGAACGGTGGGCAA
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
the specification. The primer sets can be used in gene therapy. The primers are useful for synthesising polynucleotides, in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length
                                                                                                                                                 the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5 end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3 end sequence, where the oligonucleotide which comprises a 1 east 15 nucleotides and the combination of the 5 end sequence/3 end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and the specification.
                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3093
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Best Local Similarity
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson(s disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
                                                                                                                                                                                      The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                    Tang
Wang
Zhao
                                                                                                                               assays for receptor activity, arthritis and C.N.S disorders.
Note: The sequence data for this patent did
                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and such as central nervous
                                                                                                                    specification.
                                                                                                                                                                   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                           Claim 1;
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DB; AAM42079.
 TGTGGGTGTGGACGTTGGAACAGGCAGTGTCCGTGCAGCTCTGGTGGACCAGAGTGGGGT
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Wang Z
Zhou
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2000US-0553317.

2000US-05598042.

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2000US-0663450.

2000US-0663191.

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2000US-0727344.
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Wehrman T,
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Xu C,
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TCTGCTATCCCATGCCACAGAAAAATCACGACTACGCGGGGGGAGCGGAAGCCGCGTGGA

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                   The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5 end sequence and an oligonucleotide comprising a sequence complementary to the sequence and an oligonucleotide comprising a sequence complementary to a
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  polynucleotide
                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                               full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                        and/or diagnosis of the
full-length cDNAs -
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02-MAY-2000;
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27-AUG-1999;
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Wakamatsu
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C, Otsuki
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gene

cytostatic;

cancer; tumour; gene;

gene expression;

mapping;

tissue

profiling;

Homo

sapiens. therapy;

(CHIR) (HYSE-)

CHIRON CORP HYSEQ INC.

16-AUG-2000; 16-AUG-2001; 21-FEB-2002. WO200214500-A2

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Lamson G, Scott EM,
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ang G, Kassam A,
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Pot D, Lai
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Best Local S
Matches 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. ESTs sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends; and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                           1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is one of a large number of 5' ESTs dermRNAs encoding secreted proteins. An ORF has been identified sequence. The 5' ESTs were prepared from total human RNAs or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' obtaining cDNAs and genomic DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                   153
                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity nes 179; Conserv
                                                                                                                                                                                                                                                                                          93
TATTCGCATTGGTCATCATATTGTTTCTCCCGGAACACCTTGTGGAAATGGTTTAACAGC
                                                                                                                                                                                                                                                                                                                                           CTACGAACGTGCCGGACAATTTTTCGATCTGGCCGATTTTCTGACCTGGCGGGCTACCGG 1388
                                                                           AGGCTGGGACGACAGTTTCTGGAAAATGATTGGTTTGGAAGACTTTGTTGCAGATAATTA
                                                                                                                               TCGCTGGGATCCAGATTATTTCCGCACCATTGGCCTTGCAGAGTTAGCGGATGAAGATTT
                                                                                                                                                                                   TGTCACAGCACGGTCTCTCTGCTCCCTGGTGTGTAAGTGGACATATTCAGCA---GAGAA
                                                                                                                                                                                                                                      CTGGGATAAGGCGGGACATTTCTTTGATCTCCCGGACTTCTTATCGTGGAAGGCAACAGG
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enomic DNAs that correspond to 5'ESTs and for
gene therapy and chromosome mapping procedures
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J. No. 2e-16;
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                      the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH3629 to AAH13632
                                                                                                                                                                                                                             the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprision a security.
                                                                                                                                                sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the full-length cDNAs defined in the specification, and for the defined and/or diagnosis of the abnormality of the proteins encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                             of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                       Claim 1;
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            represent oligonucleotides,
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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T, Wakama
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              all of which are used in
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Otsuki
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Best Local
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                                                                                                                                                                                         Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1794
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                                                                                                                                                                               metabolic
                                                                                                                                                                                                                                                          Aspergillus
                                                                                                                                                                                                                                                                                   13-MAR-2001
                                                                                                                                                                                                                                                                                                               AAF11917;
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         OVON (OVON)
                                                  22-MAR-1999;
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                                                                                                    28-SEP-2000
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                                                                                                                                                    Aspergillus
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Local Similarity 48.4
hes 257; Conservative
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            NORDISK BIOTECH
NORDISK AS.
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                                                                                                                                                                                                                                                                                   (first
                                                  99US-0273623
                                                                                                                                                                               engineering;
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                                                                                                                                                                              al stress; spore morphogenesis;
catabolic pathway engineering;
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Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be dentified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 88;
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                                                             TTCTGACCTGGCGGCCTACCGGTGATTTAGCGCGCTTCAGTATGCACTGTTACCTGTAA 1424
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TGAAAGAAATATGCCAGAGATCTACGAACGTGCCGGACAATTTTTTCGATCTGGCCGATT 1366
                                                                                                                                                                                                                                                                                                            TGCTGAACTACGTCGGTGGTAAAATTTCGCCTGAAATGGAAAACACCGAAAATTCTCTGGC 1306
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                                                                                                                                                                                                                                                                        TGCTTCGTTACGTTGGTGGGAAAATGTCCATTGAAATGGAGATTCCCAAGGTCCTGTGGC 254
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1: /cgn2_6/ptodata/1,

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3971
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   /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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US-09-453-702B-15
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US-09-134-001C-183
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                                                                                                                                                                                                                                                                                                    FEATURE:
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1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.2	1.3	1.3	<u>.</u>
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,,	-	Sequence 1, Appli	Sequence 78, Appl	Sequence 7, Appli	Sequence 1594, Ap	Sequence 1, Appli	Sequence 14, Appl	Sequence 1, Appli			Sequence 64, Appl	Sequence 50, Appl	Sequence 723, App	Sequence 1988, Ap	Sequence 13, Appl	Sequence 8, Appli	sequence of, Appr

ALIGNMENTS

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US-09-134-001C-183
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SEQ ID NO 183
LENGTH: 1401
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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LOCATION: (157)
OTHER INFORMATION: Identity of nucleotide
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ATTGTCTTTCATGTGTTGTTCCTGATTTTCGGCCCTGGAGCAGCAGAAATACACATTAATG
                                              TGCGTATTCCATGTTCTGGTCTTTGGATTAGGACAGGCAAACTATGGGTTAATC
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RESULT 2
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US-09-134-001C-1560; Sequence 1560, Application US/09134001C; Patent No. 6380370; GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al; TITLE OF INVENTION: NUCLEIC ACID AND AN; TITLE OF INVENTION: EPIDERMIDIS FOR DI
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                                                                          US/09134001C
   AMINO ACID SEQUENCES RELATING DIAGNOSTICS AND THERAPEUTICS
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FILE REFERENCE: GTC, 007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS!: 5674

SEQ ID NO 1560

LENGTH: 696
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1560
                                                                                                                                                                                                                                 US-09-385-028-22/c
                                  HAPPLICANT: AShish S.
TITLE OF INVENTION: F
PATENT NO. 6232106
TITLE OF INVENTION: F
NUMBER OF SEQUENCES:
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Best Local S
Matches 255
                                                                                                                                                                                            Sequence 22, Application US/09385028 Patent No. 6232106
                                                                                                                                                                          GENERAL INFORMATION:
CORRESPONDENCE ADDRESS: ADDRESSEE: JACOBSON,
                                                                                                                                  APPLICANT:
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Local Similarity | 45.2%;
nes 255; Conservative
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                                                                                                              Kwamena A Aidoo
Ashish S. Paradkar
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25
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                                                                                              DNA Sequence
  PRICE,
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Pred. No. 5.2e
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Best Local Similarity
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APPLICATION NUMBER: US 08/790
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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MOLECULE TYPE:
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CURRENT APPLICATION DATA:
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TELEPHONE: (202)
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CLASSIFICATION:
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                              TACATGACCCGGGCGGCCCTTCCCCCATCTGCT----GCGCAGCAAGGGCACCGTGGTGCAG
                                                                                                                                                                                             GAGGACGCCGACCACCGACTGGACCCGGATGATCGACCACCAATCTCCTGGGCCTGATG
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                                                                                                                                                                                                                                                            GCGCTGGGCGGCCTCGACATCCTCGTCAACAACGCCGGGATCATGCTGCTCGGCCCGGTG
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 TTCGGTGTGAACGCGTTCAGCGAGACGCTGCGCCAGGAGGTCACCGAGCGCGGGGTGCGG
                                                              ATGTCCTCGATCGCGGGCCGGGTGAACGTCCGCAACGCGGCCGTCTACCAGGCCACGAAG
                                                                                                                                                         CGCTGTGTCCGTGCAGTCCTGCCGCATATGATTGCGCCAGAGGTCGGGCGATATAATTTTT
                                                                                                                                                                                                                                                                                                                                                          CTGCAACTCGATCTCTTCAATAATCAGCAAGTCGATAACATGCTGGCGGACATTATCGAA 350
                                                                                           ACCAGTTCCATCGCGGCGTCGTTCCGGTTATCTGGGAACCGATCTACACCGCGTCCAAA
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Pred. No. 1e-11;
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US-09-385-028-13/c
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AFFLICANT: Awamena A Aidoo
TITLE OF INVENTION: | DNA Sequence Encoding
Patent No. 6232106
TITLE OF INVENTION: Acid Bian
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 279; Conserv
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                                                                                                                                                                                                                 11333 ATGCCATCCGCACTCCAGGGGAAAGTCGCGCTCATCACGGGCGCGGGCTCGGGCATCGGC 11274
 11153
                                                                                                                                           11273 GAGGCCACGGCCCGCGCCTGGCCGCCGAGGGCGCCGTGGCCATCGCCGCGCGCCGG 11214
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APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
                                  291
                                                                                                                                                                             120 ATGAATACTCCCCTTAATGGCAAAGTTGCAGCTATCACTGGCGCTGCGTCAGGTATTGGC 179
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                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
CTCGAACTCGACGTCGCCGACCGGCAGGGGGGTGGACGCCGCCGTCGCCTCCACCGTCGAG 1109
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                    CTGCAACTCGATCTCTTCAATAATCAGCAAGTCGATAACATGCTGGCGGACATTATCGAA 350
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                                                                     GTCGAGAAGCTGCGCGCCCTGGGTGACGAGCTGACCGCCGCGGGGCGAAGGTCCATGTC 11154
                                                                                                        GGCGACAAACTGCACAAGATTGTCGCTGAGTT----AGGCGAAAAACGCGTACGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (202) 39305350
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                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
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                                                                                                                                                                                                                                                                                                        1.78;
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                                                                                                                                                                                                                                                                                       Score 68.8; DB 4;
Pred. No. 6.9e-11;
0; Mismatches 297;
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                                                                                                                                                                                                                                                                                           297;
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US-09-385-028-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application Patent No. 6232106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
                                                                                                                      TELEFAX: (202) 39305350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (202 638-6666 TELEFAX: (202) 39305350
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Bullding, 400 Seventh Street,
                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
HYPOTHETICAL:
              TOPOLOGY: 1
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                                                  STRANDEDNESS:
                                                                                                                                                                                                             REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                            FILING DATE
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US-09-453-702B-15
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                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.7%; | Score 68.8; DB 4; Best Local Similarity 47.4%; | Pred. No. 8.3e-11; Matches 279; Conservative 0; Mismatches 297;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 incl
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
                                                                                                                                                                                                                         Welch, Rod | TITLE OF INVENTION: No. 6365723el Sequences NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blattner, Frederick R.
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                                                                                                                                                      STREET: 1 Sou
CITY: Madison
                                                                                             COUNTRY: US
ZIP: 53701-2113
                                                                                                                                      STATE: WI
                                                                                                                                                                                          ADDRESSEE: Quarles & Brady
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Nicole T.
                                                                                                                                                                                                                                                                                       Plunkett,
                                                                                                                                                                          1 South Pinckney Street
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CURRENT APPLICATION DATA:

CORRESPONDENCE ADDRESS:

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US-09-221-017B-383/c
US-09-221-017B-383/c
; Sequence 383, Application US/09221017B
; Patent No. 6444799
; Patent No. 6444799
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                                                                                                                          RESULT 7
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GI
NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                             1124
                                                                                                                                                                                                                                                 1064
                                                                                                                                                                                                                                                                                                                 1004 GTGGGGAATTGGCGCTGTACTTCCGGTGATGGAAGCACAGGGTTCCGGTCAGATAATCAA 106:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           884 TAGCTGGGGGGGAGTTGATGTTCTTATCAATAATGCGGGCGTTATGCCGCTTTCACCGCT
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NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
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                                                                                                                                                                                               ATTTGCCGTTCAGGC 604
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                                                                                                                                                                                                                                                                              TACCAGTTCCATCGCGGGCGTCGTTCCGGGTATCTGGGAACCGATCTACACCGCGTCCAA 589
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                                                                                                                                                                           ATTTGCAGTACGGGC 1138
                                                                                                                                                                                                                                               TCTTGGTTCTATTGGTGCCCTTTCTGTTGTGCCCCACAGGCGCAGTCTATTGTGCATCAAA 1123
                                                                                                                                                                                                                                                                                                                                                   TCGCTGTGTCCGTGCAGTCCTGCCGCATATGATTGCGCAGAGGTCGGGCGATATAATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
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47.78;
 P. GINGIVALIS NUCLEOTIDES AND USES THEREOF 1120
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Pred. No. 1.7e-10
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US-09-221-017B-383
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Best Local Similarity
Matches 176; Conserv
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                                                                                                                                                                                                                                                       1370 AGCACATACAGTGGTGGÁACAGATCAAGGCTGACTTCGGTCGGATCGATATTTTGGTGAA 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
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                                      1190
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ORIGINAL SOURCE:
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LENGTH: 5395 base pairs
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NAME: Monroy, Gladys H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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755 PAGE V
560 TATCTGGGAACCGATCTACACCGCGTCCAAATTTGCCGTTCAGGCATTCGTACACACTAC 619
                                                                      500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid | STRANDEDNESS: double
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/AU98/01023 FILING DATE: 10-DEC-1998
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                                    GATGGGACAGCGCACCGGCAGTATCATCAATATGGCTTCTGTGGTAGGTGTATCAGGCAA 1131
                                                                                                          CGTGATCAACGTTAATCTGAAGTCAGCGTTCAACATGATCCATGCCGTGACTCCCATCAT
                                                                    GATTGCGCAGAGGTCGGGCGATATAATTTTTACCAGTTCCATCGCGGGCGTCGTTCCGGT 559
                                                                                                                                          TGTGTTAAATCTGAATATAAATGCGGCGTTTCGCTGTGCCGTGCAGTCCTGCCGCATAT 499
                                                                                                                                                                              CAATGCCGGTATTACTCGCGATGGCCTTATGATGCGTATGACCGAGCAACAATGGGATGC 1251
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94304-1018
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Pred. No. 2.3e-07;
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US-08-793-035-2
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                                                                                                                                     Query Match 1.4%;
Best Local Similarity 43.1%;
Matches 269; Conservative
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                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB95
FILING DATE: 17-JUL-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Fentem, Phillip A.
TITLE OF INVENTION: B-Ketoacyl ACP
TITLE OF INVENTION: Brassica Napus
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CORRESPONDENCE ADDRESS:
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   269
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                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Arnold White & Durkee
                              CAGGTATTGGCCTGCAATGTGCAAAAACGCTGCTCGATGCAGGAGCAAAGGTAGTATTGA 228
                                                                                                   CTGTGCCCTCTATGAATACTCCCCTTAATGGCAAAGTTGCAGCTATCACTGGCGCTGCGT 168
AAGCTATTGCTCTTTCCTTGGGCAAAGCTGGCTGCAAGGTCTTGGTGAACTATGCTAGGT
                                                                 CTGTTCCGAAAGTGGAGTCTCCGGTGGTCGTTGTGACTGGTGCTTCGAGAGGGATTGGTA 268
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Chase, Dianne
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                                                                                                                                     Score 56; DB 3;
Pred. No. 1.9e-07;
0; Mismatches 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DM PC COMPOSIBLE
COMPUTER: PC POS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chase, Dianne
APPLICANT: Elborough, Keiran
APPLICANT: Fentem, Phillip A
TITLE OF INVENTION: B-Ketoacy
TITLE OF INVENTION: Brassica
                                                                               FILING DATE: 28-JUL-
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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77210-4433
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STREET: F...
ATTY: Houston
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                                                  FILING DATE:
                                                                 APPLICATION NUMBER: GB 9414622.2
                                                                                                                                         APPLICATION NUMBER: US/08/793,035
                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Arnold White & Durkee STREET: P.O. Box 4433
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                                                                                                                           US-08-594-808B-6
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Best Local Similarity
Matches 269; Conserv
                                                                                       Sequence 6, Application US/08594808B Patent No. 5804423
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                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1185 base pair
TYPE: nucleic acid
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TELEPHONE: 713.787.1400
                                    APPLICANT:
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                    APPLICANT:
 APPLICANT:
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TOPOLOGY: li
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Hollenberg, Cornelies P
                              Klasen, Ralf
Bringer-Meyer, Stephanie
                   Sahm, Hermann
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Best Local Similarity 46.6%;
Matches 215; Conservative
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TELEX: 620428
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Myers, Jonathan E
REGISTRATION NUMBER: 26,963
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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CORRESPONDENCE ADDRESS:
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                                                                                                                                              559
                                                                                                                                                                                                                                                                                                                                                                                                          207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 GCAGCTATCACTGGCGCTGCGTCAGGTATTGGCCTGCAATGTGCAAAAACGCTGCTCGAT
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CLASSIFICATION: ,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: 718/601-1099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/594,808B
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                                                                                                                                                                                                                                            CAAGTCGATAACATGCTGGCGGACATTATCGAACTGGCGGGTGGGCTGGATATTTTTCAT
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                                ATGATTGCGCAGAGGTCGGGCGATATAATTTTTACCAGTTCCATCGCGGGCGTCGTTCCG
                                                                                                                                                                                                                                                                                                                                                                     TACGGGGCTGAGGTTGTCCTGAATGGCCGGAATGCTGAAAGTCTGGACTCTGCGCAGTCC
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ATGATTCCCCGCGGACGGGCAAGATCGTCAATATCTGTTCCGTCCAGAGTGAACTCGCC
                                                                       GATCTGATGTCAACCAATGTCAACGCGGTTTTCTTCGTCGGGCAGGCGGTGGCGCGCAC
                                                                                                       CGTGTGTTAAATCTGAATATAAATGCGGCGTTTCGCTGTGTCCGTGCAGTCCTGCCGCAT 497
                                                                                                                                              AATAATGCCGGGATACAGCGCCGAGCGCCTCTGGAGGAGTTTTCGCGCAAGGACTGGGAT
                                                                                                                                                                               GCCAATGCAGGCGCTTATATTGGCGGCCCAGTGGCTGAAGGTGATCCAGATGTCTGGGAT 437
                                                                                                                                                                                                                       GGGTTCGAGGCGGAAGGATTGAAAGCCAGTACGGCGGTTTTCGATGTGACGGATCAGGAT
                                                                                                                                                                                                                                                                                                                               ATTGTCGCTGAGTTAGGCGAAAACGCGTACGCGCTGCAACTCGATCTCTTCAATAATCAG
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Pred. No. 1.2e-06;
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US-09-026-482B-1
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Best Local :
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/026
FILING DATE: 02/19/98
ATTORNEY/AGENT INFORMATION:
NAME: ALWAN, JOY
REGISTRATION NUMBER: 40486
REFERENCE/DOCKET NUMBER: S-87
TELECOMMUNICATION INFORMATION:
TELEPHONE: 630-252-2179
TELEFAX: 630-252-2779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PAUL A. GOTTLIEB, AGCTT ADDRESSEE: DEPARTMENT OF ENERGY ADDRESSEE: GC-62 (FORSTL) MS-6F-067 STREET: 1000 INDEPENDENCE AVE. S.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                                                                                       TGGATATTTTTCATGCCAATGCAGGCGCTTATATTGGCGGCCCAGTGGCTGAA------G
ATCGCTTCCATGATTTTGAACGCACCATGCAGCTGAATTACTTTGGTGCGGTACGTTTAG
                                                                                                                                                    TCTTCAATAATCAGCAAGTCGATAACATGCTGGCGGACATTATCGAACTGGCGGGTGGGC 363
                               GTGATCCAGATGTCTGGGATCGTGTTAAATCTGAATATAAATGCGGCGTTTCGCTGTG 477
                                                                                                                                 TGACTGACATGAATGCGATTGACCAGTTATCACAACAAATTATGGCCAGTGTCGATCATG 634
                                                                                                                                                                                                                      ACAAGATTGTCGCTG-----AGTTAGGCGAAAAACGCGTACGCGCTGCAACTCGATC 303
                                                                                                                                                                                                                                                                                                     TAAAAGGTAAAGTGGCTTTGATCACTGGTGCATCTAGTGGAATCGGTTTGACGATTGCAA 454
                                                                  TCGATTTCCTGATCAATAATGCAGGGCGTTCGATTCGCCGTGCCGTACACGAGTCGTTTG
                                                                                                                                                                                                   AAGAAGTGAAAGCTGCAATTGAACAGCAAGGGGGGACAGGCCTCTATTTTTCCTTGTGACC
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                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 4.1e-06;
0; Mismatches 243
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RESULT 13
US-09-296-284-66
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; ORGANISM: Gluconobacter suboxydans
US-09-296-284-67
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US-09-296-284-67
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CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87 |
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 67
LENGTH: 634
                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                        Sequence 66, Application US/09296284A Patent No. 6204040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 67, Application US/09296284A Patent No. 6204040
                                                   APPLICANT: Choi, Eui-Sung | APPLICANT: Rhee, Sang-Ki | APPLICANT: Lee, Eun-Hae | APPLICANT: Lee, Eun-Hae | TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, TITLE OF INVENTION: and Methods of Use Thereof FILE REFERENCE: 1533.0870000
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CURRENT APPLICATION NUMBER: US/09/296,284A CURRENT FILING DATE: 1999-04-22 NUMBER OF SEQ ID NOS: 87
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APPLICANT: Lee, Eun-Hae
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les 125; Conser
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                                                                                                                                                                                                                                                                                                       CATCCAA 258
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Pred. No. 2
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2.8e-06;
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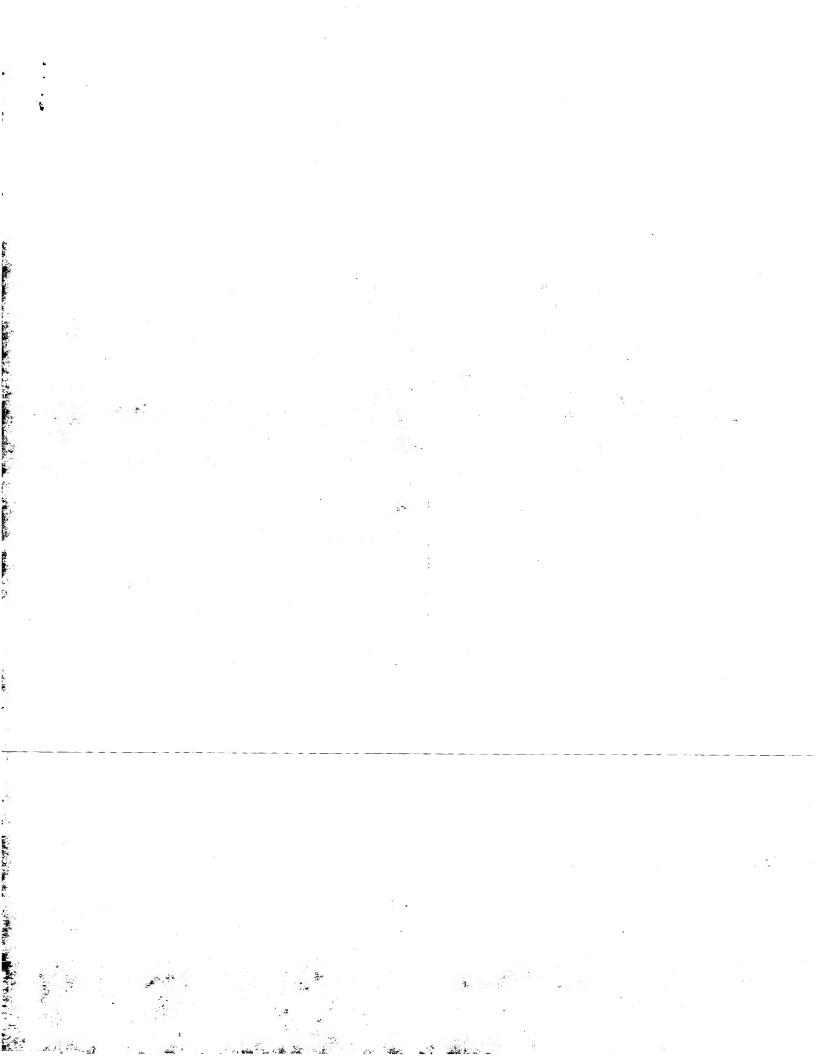
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Sequence 65, Application US/09296284A
Patent No. 6204040
GENERAL INFORMATION:
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; ORGANISM: Gluconobacter suboxydans
US-09-296-284-66
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LENGTH: 734;
TYPE: DNA; ORGANISM: Gluconobacter suboxydans
US-09-296-284-65
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                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Choi, Eui-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: 1533.0870000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 199-04-22
NUMBER OF SEQ ID NOS: 87
NUMBER OF SEQ ID NOS: 87
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NUMBER OF SEQ ID NOS: 87
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                                                                                                                                                                                                                                                                             Match 1.3%;
Local Similarity 50.6%;
les 125; Conservative
                                                                 GCCCAGTGGCTGAAGGTGATCCAGATGTCTGGGATCGTGTTAAATCTGAATATAAATG 462
TCATCAACATCAGTTCCCAGGCCAGCTCTGTCGCGCTGATTGACCATGGTGCTTACGTCG
                                TAATTTTTACCAGTTCCATCGCGGGCGTCGTTCCGGTTATCTGGGAACCGATCTACACCG
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Pred. No. 3e-06;
0; Mismatches 122;
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Pred. No. 3.1e-06;
0; Mismatches 122;
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US-09-296-284-63
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Search completed: March 21, Job time: 186.991 secs
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LENGTH: 784
TYPE: DNA
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APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase,
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: 1533.087000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
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mes 125; Conservative
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                     2003, 11:12:44
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Pred. No. 3.3e-06;
0; Mismatches 122;
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Gapop 10.0 , Gapext 1.0
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3971
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| Cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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10 US-09-974-300-6537

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US-09-738-626-127
US-10-114-170-15
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US-09-070-927A-238
US-09-974-300-2287
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10373.549 Million cell updates/sec
                                                                                                                                                                                 Sequence 127, Appl
Sequence 15, Appl
Sequence 6500, Ap
Sequence 238, App
Sequence 2287, Ap
Sequence 6558, Ap
                                                                                                                 Sequence 99, Appl
Sequence 71, Appl
Sequence 4, Appli
Sequence 6537, Ap
                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                        Sequence 2, Appli
Sequence 11317, A
                                               Sequence
Sequence
                                                                                  Sequence 15, Appl
Sequence 13, Appl
                 Sequence
Sequence
2280, Ap
165, App
13, Appl
6029, Ap
67795, Ap
                                                                                App1
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ALIGNMENTS

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; FEATURE:
NAME/KEY: misc_feature
; LOCATION: (2565);.(3839)
; OTHER INFORMATION: ribitol transporter coding region
US-09-802-208B-2
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LENGTH: 3971
TYPE: DNA
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                                                                                                                                         Query Match 100.0%; Score 3971; Best Local Similarity 100.0%; Pred. No. 0; Matches 3971; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Arabitol or Ribitol As Positive Selectable Markers FILE REFERENCE: UGA-855R CURRENT APPLICATION NUMBER: US/09/802,208B CURRENT FILING DATE: 2001-03-08 NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Parrott, Wayne APPLICANT: LaFayette, Pe APPLICANT: Kane, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: (859)..(2463) OTHER INFORMATION: ribitol
                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: ribitol dehydrogenase coding region
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: (96)..(848)
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61 CAGAGACTATAAATTCGCCCTGGTAAAAGGATTATATGATGAATCACTCTGTGCCCTCTA 120
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1200 1200	11 CCATTGCCTGTCAGCCCGGAAGGAAGTGCAAAGCAAAATATCATTGTGTGGATGGA	114; 114;	DP QA
114 114	31 GTGGCAGGCATCGGTTTTGATGCCACCTGTTCTCTGGTGGTACTGGATAAAAACGGTGAT 	108:	D 9
108 108	21 CAGGCGGTCTGTTCATGTATTCGTAATGCGCTCACTCTGGCAGACGTTTGTGCACAAAGT 	1021 1021	p 9
102 102	31 AAAATCACGACTACGCGGGCGAGCGGAAGCCGCGTGGAACAGTCCAGGCAGG	96. 96.	Db 04
960)1 GGCAGTGTCCGCGCGCGGATTTTTGATCTCAACGGATCTCTGCTATCCCATGCCACAGAA 	90:	Дb
900	11 ATCTGTAAGGGCGCAATCATGACAATAACCAAAACCGTTATTGGTGTGATGTGGGATCA	84	Db Qy
840 840	31 TGGTGACCCGCTCGAAAAATGTCACCGTGCGAGATTTAGTGATCCTGCCTG	78: 78:	₽ Ş
780 780	21 AAGCCCTGGCAAATGGTAGCCTGATGCAACCGATTGAAGTGGCGGAATCAGTATTGTTTA 	72 72	DP Q
720 720	31 TGCTGCCAGGACCAGTAGTCACTGCCCTGCTTGATGACTGGCCAAAAGCCAAAATGGAAG 	66.	ρ δ
660	11 AGGCATTCGTACACACTACCCGCCGCCAGGTTTCTCAATATGGCGTGCGT	60	Оγ
600	11 TCGCGGGCGTCGTTCCGGGTATCTGGGAACCGATCTACACCGCGTCCAAATTTGCCGTTC	54	B 8
540 540	31 GTGCAGTCCTGCCGCATATGATTGCGCAGAGGTCGGGCGATATAATTTTTACCAGTTCCA 	4 8	рb
480 480	21 ATCCAGATGTCTGGGATCGTGTGTTAAATCTGAATATAAATGCGGCGTTTCGCTGTGTCC 	42	g 24
420 420	31 GGCTGGATATTTTTCATGCCAATGCAGGCGCTTATATTGGCGGCCCAGTGGCTGAAGGTG 	36. 36.	Db Qq
360 360	11 ATCTCTTCAATAATCAGCAAGTCGATAACATGCTGGCGGACATTATCGAACTGGCGGGTG 	30: 30:	Db Db
300 300	11 GCGACAAACTGCACAAGATTGTCGCTGAGTTAGGCGAAAACGCGTACGCGCTGCAACTCG 	24:	р Оу
240 240	11 TGCAATGTGCAAAAACGCTGCTCGATGCAGGAGCAAAGGTAGTATTGATTG	. 18: 18:	Dу
180 180	1 TGAATACTCCCCTTAATGGCAAAGTTGCAGCTATCACTGGCGCTCCGTCAGGTATTGGCC	121 121	β 6
120	51 CAGAGACTATAAATTCGCCCTGGTAAAAGGATTATATGATGAATCACTCTGTGCCCTCTA	6	Db

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2161 GTAGTGAGTAAAATATCGTTATTAGCGGCGGTGCCGGGCAGCATCCACTGGT	2041 GTAATTTGTGGCCTGGGTATGGAGCGAGATCTGGATAATTT	1861 GTTGAAGAAGCTCCGGAAATGGCACAACGTGTGAATCAGCCCCTCCCCGTCTGGC	1681 AATCTCGCGTATGTTTTCGGCACTTCTTCATGCACCATGCCATCTACCACTTCTC	1501 GAAGATTTTATTCGCATTĞGTCATCATATTGTTTCTCCCGGAACACCTTGTGGAAATGGT	1201 CGCGCCACCGAACAAGCÁGAGCGAATCAATGCCACTCACCATCCGGTGCTGAACTACGTG
GGCAGCATCCACTGGTACGACAA 2220	ATTTACTCGCCTTGTATATCGCT 2100	AGCCCCTCCCCGTTGCT 1920	TGGCATCTACCACTTCTCCCTCG 1740	ATTGTTTCTCCCGGAACACCTTGTGGAAATGGT 1560	ACCATCGGTGCTGAACTACGTC 1260

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TCTGGGCGGCATTTTTCTTTACCACTATTTTCTCTAATATTTTTTGGGGGATTGTGGCAG
              CTCCCCGTGAGAAGTTTGCAGAATTAAGTCGGGCAGTAACTTTACTTTATACCAACCGCA
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GENERAL INC. GENERAL INC.

GENERAL INC. GENERAL INC.

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengbing

APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: MUSCLEIC ACID AND OTHER MOLECULES ASSI-

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/980,352

CURRENT APPLICATION OUMBER: US/09/980,352

CURRENT APPLICATION OF EDITOR OF SEQ ID NOS: 15112

SEQ ID NO 11317

LENGTH: 417

TYPE: DNA

ORGANISM: BOS taurus

ORGANISM: BOS taurus

ORGANISM: BOS taurus

OTHER INFORMATION: Clone ID: 48-LIB34-080-Q1-E1-D8

US-09-960-352-11317
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US-09-960-352-11317
; Sequence 11317, Application US/09960352
; Patent No. US20020137139A1
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                                           Conservative
                                                     12.5%;
56.2%;
                                          Score 101; DB 10;
Pred. No. 2.7e-22;
0; Mismatches 175;
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PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 127
LENGTH: 1335
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-127
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR TILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: CCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
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APPLICANT:
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TATEISHI, NAOKO
SENOH, AKIHIRO
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Pred. No. 4.3e-12;
0; Mismatches 663;
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155 TGGATGACTCTTCAACTTCGCGGCACCCAACCAGGATTCGACGGAGTGCCAG TACAACCTCGGCGTTGGTGGCCGCTGTAGCTGTGGGACCGCTCCTGGTTGCAGTCTTCCAC TACAACCTCTCTGCGGGTATGTCTAACTTCCTGGCTCCGGCAATTGCCGTGGTGTTATTA CCACTTTCCGCAATCGCTGTCTCCCTTGATCCCAAGCACCCCGGCGCAGCGATGGCCACA AGTTTAGCGTTTTACTACATGCCGCAATACTTTGGTCA-----GAAAAAATGGGCTGGATGCGTTATTCGCTGGTTTGGTTGCCTCGGGATGGCATCA ---TACGTGAACTTGACCTTCTATGAAACGTTGTGGGTTTCCCTCGTGCTGGTGGTCATC GTCCTTTGCGCATTCATTCGCGTTGAGCAGCCAGGATTCAGTTCTGCGCCCAG CCACTGATTGGTCCAACCGGATTGATCCTGGTCATGATCGCCCTCTACCTGCTCTCCGGT CCGTGGTTTAGCACTATCGGTGTGGTCATTGCCTATACAGCATTGTATCTATTGGCCTTT CCGATGGCCGCTGTCTTCCCGGCACTGGAACCAAAACACAAAGGTGCTGCAATCTCGGTT GTTTTCGGAATCACCATCGCAGCCGGCGCACTCTTTGGTGTGTCCCTCGCGGGCTTCGTG CTCACCACTGTAATTTACGCAGTCAACCTGCCGTTCAATCCTTTCTTCGGTAGCTTCGGC GTCTGGGCGCATTTTTCTTTACCACTATTTTCTCTAATATTTTTTGGGGGATTGTGGCA GTCATTATGCCAATGATGTTTGTGGATGAACTGGGATTCACCACCTCTGAATGGTTGCAG CGTGCACGTTTTGTCACCTACATCCGCACCATCAACTCCATTCCGACCTACGCGATGGCT ACTCCCCGTGAGAAGTTTGCAGAATTAAGTCGGGCAGTAACTTTACCTTTATACCAACCGC ATTGCCATGATCTCCTTGCGTCATGTTAAAACGCCT-----GGACATATGCATAATTTA CGGTATATTCAGTAGGGATCGGTGTTGCTGGCAGTTATATTCCCAGTTTTACGATACCGA TCCTGCTGTTTTACGGGATTCGTGGTTTAGCGTATCCGCTATTTCTCTACTCATTTATCG CTGGGGTAGTAGCGGAAATCATCACGCCGCAAAAAACCATGCTGATTGGTTTTGTCCTAT AACTACTGGATGGCAATGATTCCGGCGATTGCTCTGGGAACTTTTGTTGCTGCATTTGTG CTCGCGTTGGTTTACTTCATTCCGATGTTCGGCGTTCAGGCTGGCATGTCCAACGGTGTC GACCGCCACGGTTGGGCACGAACTGTGTTCTGGGGCGGATCAATCGGTGGCGCAGTCACC GTGTTCTTCCCATCATTTTTCACTGACGATCTGAAGTGGCAGCTAAGCTGGTTCCTCATC **AATATTTTTCTCTCCAGTATTGTGCGCATTATAAATACCTTATCGTTTATTCGGTTTTGCG** AACCCCGACGATGTGAAGCAAACACTTGGCCAGGGCTTCAAACTTCTGCGCAATGATCGA TTATGGGTGAAATGGGAACCTTATGGCTGGCACTGGCGTTCTGCTTTGCTGGCGGT-GTC TTGCCTTCTCTGCAGGTCTTCCTACCTTGGGTGCGCTGGTTGCCACCATTTCCATGCAG-TCGTTATTATTCATAACGTGCGTAGCGAAAATTCCAGTTCTGCTCTGGGTTGGTACTGGG TCTTCCTTGCTTATGGTCTCCGCGGCTTTGGTTATCCATTCTTCGCCTACGGATTCTTGG GGTGCGTATTCCATGTTCTGGTTTTGGTCTTTGGATTAGGACAGGCAAACTATGGGTTAA 2886 CGGCGGCACTTTCGGACCTGTGGGGTCCACGAAAAGTGATGATCCTCGGTGCTTCAATCT GGATCGTCTTTGAGCTGATCTTCCTCACCGTGGCACTGACCACCGACCATACTTGGTTGA CCCTCGCGGGAACCCTGGTGACTGTTTACGGTGTTGCCGTGGCGATCGCAGCATTCTTCG 1282 3810 ----c 1170 3758 3638 3578 930 3479 870 3419 750 3299 3239 3179 3066 3006 2946 1050 3518 810 3359 570 990 690 630 513 454 394

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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      Matches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (608) 251-1
INFORMATION FOR SEQ ID NO: 15
                                                                                                                                                                                                                                                  644
                                                                                                                                                                                                                                                                   119 TATGAATACTCCCCTTAATGGCAAAGTTGCAGCTATCACTGGCGCTGCGTCAGGTATTGG 178
 350
                                                                                                                                                                              704
                                                                                                                                                                                                            APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/114,170
EILING DATE: 01-Apr-2002
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Welch, Rod TITLE OF INVENTION: No. US20030023075Alel Sequences of E. coli 0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Blattner, Frederick R
ACTGGCGGTTGGATATTTTTCATGCCAATGCAGGCGCTTATATTGGCGGCCCAGT 409
                                                                                                                         AGGCGACAAACTGCACAAGATTGTCGCTGAGTT-----AGGCGAAAACGCGTACGC 289
                                                                                                                                                                           GGAAGGTATTGCCAGAGAGCTTGGAATGACAGGTGCAAAGGTTTTACTGGGAGCACGCAG
                                 GCGGGAGTTGGATGTCACAGACCGACAGTCCATGGCCGATTTCGTGCAAGCAGCGCTGGA
                                                                     GCTGCAACTCGATCTCTTCAATAATCAGCAAGTCGATAACATGCTGGCGGACATTATCGA 349
                                                                                                      AGTTGAGCGTATCGAAGCCATTGCAACCGAAATCTGCCGCGCAGGAGGAATTGCTAAAGC
                                                                                                                                                                                                                                                TTTGAAGGAGAACGTAATGGATAAGGTCATATTAATTACCGGCGCATCAAGTGGTATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Seay, Nicholas J
REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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Pred. No.
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BER: 960296.95017
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                                                                                                                                                                                                                                                                                                                  SEQ ID NO 6500
LENGTH: 789
                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6500, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/206,848
PRIOR TILING DATE: 2000-05-3
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                FEATURE:
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124 ATACTCCCCTTAATGGCAAAGTTGCAGCTATCACTGGCGCTGCGTCAGGTATTGGCCTGC 183
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                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/253,625
                                                        ATTTTCAATTAGATGGAAAAGTAGCGTTAATTACAGGTGCTGTTTATGGGATTGGCTTTG 79
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                                                                                                                                212;
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Zyskind, Judith W.
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Yamamoto, Robert T.
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                                                                                                                                Conservative
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                                                                                                                                                 1.68;
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Pred. No. 4.2e-10;
0; Mismatches 214;
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RESULT 6
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                                                                                        TELEFAX: (301) 30 INFORMATION FOR SEQ ID NO:
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                                                                                                                                         APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. HOOVET
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
MEDIUM TYPE: UD Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                   ENCE CHARACTERISTICS:
LENGTH: 29729 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 9410 Key West Avenue CITY: Rockville
                      STRANDEDNESS:
                                                                                                                              TELEPHONE: (301)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Maryland
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Patrick J. Dillon
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; TYPE: DNA; ORGANISM: Bacillus licheniformis US-09-974-300-2287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-974-300-2287
                                                                                                                                 Query Match
Best Local Similarity
Matches 199; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2287, Application US/09974300 Patent No. US20020146721A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows SEQ ID NO 2287
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Expression FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/279,526 PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Berka, Randy M. APPLICANT: Clausen, Ib Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15623 ATTTTCAATTAGATGGAAAAGTAGCGTTAATTACAGGTGCTGTTTATGGGATTGGCTTTG 15682
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                                                                                  234 CGGGAAGGCGACAAACTGCACAAGATTGTCGCTGAGTTAGGCGAAAACGCGTACGCGCTG 293
                                          34 ATCGCCCTGGACCTGGCGAAAAAACGGAGCAAATGTCGTCGTCAACTACGCGGGAAATGAA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
mes 212; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGTCCGTGCAGTCCTGCCGCATATGATTGCGCAGAGGTCGGGCGATATAATTTTTACCA
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                                                                                                                                                         Score 63.4; DB 10; Pred. No. 6.9e-10;
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; ORGANISM: Bacillus clausii
US-09-974-300-6558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6558
LENGTH: 744
                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6558, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CORRENT APPLICATION NUMBER: US/09/974,300
CURRENT APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
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                                                                                                                                                                                                                           327 AACATGCTGGCGGACATTATCGAACTGGCGGGTGGGCTGGATATTTTTCATGCCAATGCA 386
                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                     267 GAGTTAGGCGAAAACGCGTACGCGCTGCAACTCGATCTCTTCAATAATCAGCAAGTCGAT 326
                                                                                                                                                                                                                                                                                                                                            Local Similarity nes 227; Conserv
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CAGAGGTCGGGCGATATAATTTTTACCAGTTCCATCGCGGCGTCGTTCCGGTTATCTGG
                                     GATACCAACTTAAAAAGGGGTGTTCCATTGCGCGAAAGCAGTCAGCCGGCAAATGATGAAA 390
                                                                                                                                                                                                                                                                 GCGCTTGGCCAAGAGGCGTTTGCGTATCAGGCTGACGTTGCCTCCAAAAGGGAAGTCGCA 210
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                                                                                                              GGCATTACGCGCGATAACTTGCTAATGAGAATGAAAGAAGACGATTGGGATGCCGTCATT
                                                                                                                                                    GGCGCTTATATTGGCGGCCCAGTGGCTGAAGGTGATCCAGATGTCTGGGATCGTGTTTA
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Pred. No. 1.1e-09;
0; Mismatches 273;
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US-09-712-363-99
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CÜRRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR PILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 99
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DITERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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                                                                                                                                                                                                                                                                                                                                             LENGTH: 80
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 GAATTGGCAGGGCGAGGCATTCTTGTCAATGCGGTGGCGCCCGGCTTTATTACGACAGAT 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 CAACGTGCTGGCAGAATCATCAATGTCTCGTCTGTCGTTGGCGTAATGGGTAACGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/165,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/126,593 FILING DATE: 1999-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/134,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/165,124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                        ATGATTGCGCAGAGGTCGGGCGATATAATTTTTACCAGTTCCATCGCGGGCGTCGTTCCG
                                                                                                 CGTGTGTTAAATCTGAATATAAATGCGGCGTTTCGCTGTGTCCGTGCAGTCCTGCCGCAT 497
                                                                                                                                             GCCAACGCGGGTACCGCGACATTCGGCCCGATCGCATCGCTCGATCTTGCCGGCGAAAAG
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1999-11-12
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Pred. No. (
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US-09-070-927A-4/c
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US-09-813-453A-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF TITLE OF INVENTION: ANTIBIOTICS FILE REFERENCE: OGZ-001
CURRENT APPLICATION NUMBER: US/09/813,453A
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/227,860
PRIOR FILING DATE: 2000-09-24
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 77
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APPLICANT: Patterson, Thomas A.
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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les 165; Conserv
                                                                                                                                             GCGTGTGGGTGCGGTGCCAGGACCAGTAGTCACTGCCCTGCTT 692
                                                                                                             TTATGTGACAACAGTCAACCCGGGCCCGATTCAGACGGACTTTTTT 984
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                                                                                                                                                                                                                                                       CAATATCGCCTCTCAAGCGGGGAAAATCGCCACACCGAAGTCTAGCCTGTATTCCGCGAC
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Pred. No. 1.3e-06;
0; Mismatches 181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 218; Conserv
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GENERAL INFORMATION:
APPLICANT: Charles A:
Patrick J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        3077
                                                                                                                                                                                                                                                                  3017 AAAAAAGAACTTCCTGAAGCAACGATTCTCGTGCAACAAGCAGATGTAACGAAAGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3137 AAAGTTATTGTTATCATGGGCGCTTCCAGTGGCATCGGTGAGGCAACAGCCCGTTTACTT 3078
                                    438 CGTGTGTTAAATCTGAATATAAATGCGGCGTTTCGCTGTGTCCCTGCAGTCCTGCCGCAT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 AAAGTTGCAGCTATCACTGGCGCTGCGTCAGGTATTGGCCTGCAATGTGCAAAAACGCTG 200
                                                                                                                                                                                                                      318 CAAGTCGATAACATGCTGGCGGACATTATCGAACTGGCGGGTGGGCTGGATATTTTTCAT 377
                                                                                                                                                                                                                                                                                                                                                                                                      201 CTCGATGCAGGAGCAAAGGTAGTATTGATTGACCGGGAAGGCGACAAACTGCACAAGATT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. HOOVET
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
addresses: Address Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301);309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
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MEDIUM TYPE: DISACTIC, 3.50
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Vel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982\,
                                                                                     AACAATGCAGGAGTTATGCCAACGGCGCCTCTTATTGAAGCACCAAAAGGAGAATGGCGT
CAAATGCTAGATATTAATATTATGGGTGTTTTAAATGGCATTGCGGCAGTTCTTCCAATT
                                                                                                                               GCCAATGCAGGCGCTTATATTGGCGGCCCAGTGGCTGAAGGTGATCCAGATGTCTGGGAT 437
                                                                                                                                                                             GAAGTTCAGCGTGTAATCAAGCTTACAATGGAAAAATATGGACGAATTGATGTTCTTTT
                                                                                                                                                                                                                                                                                                              GTCGCTGAGTTAGGCGAAAACGCG---TACGCGCTGCAACTCGATCTCTTCAATAATCAG 317
                                                                                                                                                                                                                                                                                                                                                          GCCAGAAAAGGAGCGAAGTTAGTCATTGCAGCACGTCGACAAGAACGTTTAATTGCTATA 3018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
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Pred. No. 2.1e-06;
0; Mismatches 249;
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498

ATGATTGCGCAGAGGTCGGGCGATATAATTTTTACCAGTTCCATCGCGGGCGTCGTTCCG

557

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US-09-974-300-6537

; Sequence 6537, Application US/09974300

; Patent No. US20020146721A1
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; ORGANISM: Bacillus clausii
US-09-974-300-6537
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TITLE OF INVENTION: Methods For Monitoring Mu.
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
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RESULT 13
US-09-885-303A-15
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 6537
LENGTH: 537
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Best Local Similarity 45.1%;
Matches 202; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Berka, Randy M
APPLICANT: Clausen, Ib G
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                                                                                                                                                                                                                                                      301
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                                                                                                                                                                                            TCACTGCCCTGCTTGATGACTGGCCAAAAGCCAAAATGGAAGGAGCCCTGGCAAATGGTA 738
                                                                                                                                                                                                                                                  TGGCGCGGAATTGGCAGGGCGAGGCATTCTTGTCAATGCGGTGGCGCCCCGGCTTTATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGTCATTGATACCAACTTAAAAGGGGTGTTCCATTGCGCGAAAGCAGTCAGCCGGCAAA
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Pred. No. 7e-07;
0; Mismatches 246;
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; NAME/KEY: CDS |
; LOCATION: (62)..(1000)
; NAME/KEY: modified base
; LOCATION: (56)
; OTHER INFORMATION: 'N = A, C
US-09-885-303A-15
                                                                                                                                                                                                                                                                                                                     US-09-885-303A-13; Sequence 13, Application US/09885303A; Publication No. US20030032078A1
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SEQ ID NO 15
LENGTH: 1872
TYPE: DNA
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APPLICANT: TRAVIS, GABRIEL H.
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local Similarity 47.0%;
Matches 157; Conservative
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                                                              SEQ ID NO 13
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                                                                                                                                                                  APPLICANT: TRAVIS, GABRIEL H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: AND RETINAL DEGENERATIONS
FILE REFERENCE: UTSD: 758US
CURRENT APPLICATION NUMBER: US/09/885,303A
CURRENT FILING DATE: 2001-66-19
                                                                                                      PRIOR APPLICATION NUMBER: 60/263,837 PRIOR FILING DATE: 2001-01-23 NUMBER OF SEQ ID NOS: 24
                                                                                SOFTWARE: Patentin Ver.
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                      TYPE: DNA
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    ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 651 GTGGGTGCGGTGCCAGGACCAGTAGTCACTG 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         602
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Pred. No. 2.9e-05;
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GENERAL INFORMATION:

APPLICANT: Berka, Randy M.

APPLICANT: Clausen, Ib Groth

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OF INVENTION: Expression

FILE REFERENCE: 10085.500-US

CURRENT APPLICATION NUMBER: US/09/974,300

CURRENT FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 09/880,598

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/279,526

PRIOR APPLICATION NUMBER: 60/279,526

PRIOR FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 8481

SOFTWARE: FBSATSEQ for Windows Version 4.0

SEQ ID NO 2280

LENGTH: 680
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; NAME/KEY: CDS
; LOCATION: (250)..(1185)
US-09-885-303A-13
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US-09-974-300-2280
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                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 680
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.3%;
Best Local Similarity 47.1%;
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2280, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                             Ouery Match 1.3%; Score 50.2; DB 10; Length 680; Best Local Similarity 52.1%; Pred. No. 2e-05; Matches 112; Conservative 0; Mismatches 103; Indels 0
                                                                                                                                394
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                                                                                                                                                                                              334 TGGCGGACATTATCGAACTGGCGGGTGGGCTGGATATTTTTCATGCCAATGCAGGCGCTT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       612 CGTCAAAGCTGTGCTTCCAGGCATGAAGAGGAGGCGGCAGGGCCACATCGTGGTGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 GGGTGGGCTGGATATTTTTCATGCCAATGCAGGCGCTTATATTGGCGGCCCAGTGGCTGA 415
338
                       454 ATATAAATGCGGCGTTTTCGCTGTGTCCGTGCAGTCCTGCCGCATATGATTGCGCAGAGGT 513
                                                                                       278
                                                                                                                                                                       218 TCGCTGAGGCAAAACAGCGGTTTGGGCGGGGGATCGATATTTTGGTCAACAATGCCGGCGTTA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    672 CAGTGTCATGGGCCTGCAGGGTGTCATCTTCAACGATGTCTATGCAGCTTCCAAGTTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              536 TTCCATCGCGGGCGTCGTTCCGGGTATCTGGGAACCGATCTACACCGCGTCCAAATTTGC 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 TGTCCGTGCAGTCCTGCCGCATATGATTGCGCAGAGGTCGGGCGATATAATTTTTACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552 GCTCAGCCTTGCTGCCATGCAGAATGTCTTTGACACCAACTTTTTCGGAGCTGTCCGTCT 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 AGGTGATCCAGATGTCTGGGATCGTGTGTTAAATCTGAATATAAATGCGGCGTTTCGCTG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 GGGAGAAGTGGACGTGCTGGAATAATGCTGGAATGGGCCCTGGTGGGGCCCCCTGGAGGG 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          792 CCTGGTGGAGCCAGGCCCCGTGGTCACCG 820
                                                                                                            ATATTGGCGGCCCAGTGGCTGAAGGTGATCCAGATGTCTGGGATCGTGTGTAAATCTGA 453
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ATTTAACCGGCACCTTTCTCATGTGTCAGGCTGTCATCCCGGAAATGATCACGCAGGGCG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50.6; DB 9; Length 1:
Pred. No. 3.1e-05;
0; Mismatches 174; Indels
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Search completed: March 21, 2003, 15:43:42 Job time: 380.853 secs

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Title:
Perfect score:
Sequence:
                                                                                                Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                            199.4
189.2
185.8
171.4
  169.8 \\ 169.8
                                                                                                Score
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3971
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10552.182 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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  5.0
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Copyright (c) 1993 - 2003 Compugen Ltd.
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RH22404 K-EST01 AU121672	RST3707 T3 end 179972	RH30085 RE70835	BM036183 ful6h06.y BM036183 ful6h06.y BI613997 RH43270.5 BQ801483 WHE2814 H	AGENCOU RH63626	AL749866 AL749866 AK009249 Mus muscu	AI789136 uk51d10.y BI819693 603037856	BI629061 RH57864.5 AW164681 se76b09.y	AI196200 ui70b11.y BQ406350 GAEd009	AII00240 GH0/020.3 AI388552 GH19496.5 BI329415 602980145	BF218299 601881643 BG768597 602741908	BQ932942 AGENCOURT BF783891 602109920	AI527876 uj30c03.y BM646051 170006873	BI149014 602911220 BF440790 256813 MA	AZ650403 1M0520L01 BI557944 603237561	79110 30258

ALIGNMENTS

source	FEATURES											COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BI260394
 1692	Location/Qualifiers	High quality sequence stop: 692.	Plate: LLAM11263 row: p column: 13	http://image.llnl.gov	found through the I.M.A.G.E. Consortium/LLNL at:	Clone distribution: MGC clone distribution information can be	DNA Sequencing by: Incyte Genomics, Inc.	cDNA Library Arrayed by: Incyte Genomics, Inc.	cDNA Library Preparation: Life Technologies, Inc.	Tissue Procurement: ATCC	Email: cgapbs-remail.nih.gov	Contact: Robert Strausberg, Ph.D.	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	NIH-MGC http://mgc.nci.nih.gov/.	1 (bases 1 to 692)	Mammaliā; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	EST.	BI260394.1 GI:14818651	BI260394	mRNA sequence.	602969456F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5108988 5',	BI260394 692 bp mRNA linear EST 17-JUL-2001	

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SOURCE
ORGANISM
                                                                                                                                                                                                                                                       RESULT 2
BQ934625
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                                                                                                                                                                         922
AGENCOURT_8818058 NIH_MGC_18
5', mRNA sequence.
BQ934625
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 922)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                    Homo sapiens
                                                                                                                                                             BQ934625.1
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Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.4 kb. Library prepared by Life
Technologies."
149 c 204 g 168 t
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/db_xref="taxon:9606"
/clone="IMAGE:5108988"
/clone_lib="NIH_MCC_12"
/tissue_type="cervical carcinoma cell line'
/lab_host="DH10B"
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Pred. No. 9.6e-48;
0; Mismatches 226;
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Ното
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Contact: Robert St
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Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Corgan: lung; Site_1: XhoI; Site_1: XhoI; Site_2: XhoI; Site
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/db_xref="taxon:9606"
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GGTGTGTAAGTGGACATATTCAGCA---NAGAAAGGCTGGGACGACAGTTTCTGGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.linl.gov
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5', mRNA sequence
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                                                                                                                                                                                                                                                                                    /tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DHIOB (phage-resistant)"
/note="organ: liver; Vector: porm5; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAC(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6300239"
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Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 736)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                            e: LLAMI1461 row: e column: quality sequence stop: 736.
| Location/Qualiflers
/note-"Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); source anonymous pool of 3 colons, age 26 yo male, 49 female, 71 yo male colon; 46 yo male kidney, and pool stomachs, 62 yo male and 70 yo female. Library is
                                                                                                     /lab_host="DH10B"
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/clone_lib="NIH_MGC_116"
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5', mRNA sequence.
BO440371
                                   Contact: Robert Strausberg,
                                                                     Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 905)
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National Institutes of Health, M
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cgapbs-r@mail.nih.gov
Procurement: ATCC
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/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
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/db_xref="taxon:9606"
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                                                                                                                    ACAGTCCAGCCAGGAGATCTGGCAGGCGGTCTGTTCATGTATTCGTAATGCGCTCACTCT 1058
                                             CCATCCGGTGCTGAACTACGTCGGTGGTAAAATTTCGCCTGAAATGGAAACACCGAAAAT 1298
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  GCACAGTGTCCTCCAGTACGTCGGGGGGGGTGATGTCTGTGGAAAATGCAGGCCCCGAAACCT
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12786 row: k column: 06
High quality sequence stop: 726.
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National Institutes of Health, 1
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1 (bases 1 to 1069)
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/db_xef="taxon:9606"
/clone="IMAGE:5752445"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
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Kim, N.S., Hahn, Y.,
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                                                                                                                                                                                           /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: ECORI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayana-Berg method. The
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                                                                                     obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method The cDNA libraries constructed by this method are full-length enriched cDNA library."
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/db_xref="taxon:9606"
/clone="S21SNU520-19-B10"
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/cell_type="Floating aggregates"
/cell_line="SNU-520"
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  Small Genomes Sequencing Group Department of Molecular Evolution, Norbyvagen 18C, S-752 36, Uppsala, Tel: 46-18-471-4379
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                                    Junn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
plasmid inserts
                          Mouse whole genome scaffolding with paired
                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 655)
                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                     AZ650403
AZ650403.1 GI:11784856
                                                                                                                                                                                                                                                                                                                                                    AZ650403 655 bp DNA linear 1M0520L01R mouse 10kb plasmid UUGClM library Mus n clone UUGClM0520L01 R, DNA sequence.
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/clone="UUJ525"
/clone="lib="Brucella abortus random
/clone_lib="Brucella abortus random
/note="Vector: modified M13"
/note="Vector: 144 g 94 t
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/strain="2308"
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57.1%;
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Rodentia;
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Pred. No. 3.8e-34;
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                            end
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                            reads from 10kb
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1024 GCGGTCTGTTCATGTATTCGTAATGCGCTCACTCTGGCAGACGTTTGTGCACAAAGTGTG 1083
1084 GCAGGCATCGGTTTTGATGCCACCTGTTCTCTGGTGGTACTGGATAAAAACGGTGATCCA 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                           1204 GCCACCGAACAAGCAGAGCGAATCAATGCCACTCACCATCCGGTGCTGAACTACGTCGGT 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           655 GCGGTCTGCATCGCGGTCAGGGCAGCGCTTGCCGAGGCGGCTGTTCCGCGCGCAAAGCATT 596
                                                                                        GAGATCTACGAACGTGCCGGACAATTTTTCGATCTGGCCGATTTTCTGACCTGGCGGGCT 1383
                                                                                                                                   ACAGCGTGTCGCCGGAAATGCAGATGCCGAAGCTGATGTGGCTGAAGAAGAATTTGCCG
                                                                                                                                                                                   GTTTCGGTCTCCGTCACTGGCAAAGACAAGTTCGACACGATCGTCTGGCTTGACCACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                   GCCGCCATCGGGTTCGACGCCACCTGCTCGCTGGTTATCCGGGACGAAAAGGGAGAACCG 536
                                             GCAAGCTGGGCCCGCATGTCTTTCGCCTTCGATCTGGCGGATTTCCTCACCTGGAAAGCG
                                                                                                                                                                                                                                  GCAATCGTCGAGGCCGATCGGTTGACGGCATCCGGCCACCGGGTTTTTGGATTTTTGCCGGT
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High quality sequence stop: 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0520 row: L column: 01
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Utah Genome University of Utah Rm. 308, Biomedical Polyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0520L01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
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232 c
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Pred. No. 6e-33;
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    Matches
                       Query Match 3.8%;
Best Local Similarity 56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 GAAAATCCCGGTTGGCAGGCGGATTATCTC-GAACTGGCCGGGCTTGGTGATCTGAAGGA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGCACAAGCCGCGGCAGAGATGGGATTACTCCCCGGCACACCTGTCGCTGTAGGGTTA 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCGATGCCTATGCGGGTGCGCTCGGCGCGCTTGGCGGATGCCTTCGGGGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deno
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 710
    Conservative
                                                                                                         Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
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/deb_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5290478"
                                                                                                                                                                                                                                               /note="Organ: mammary; Vector: pCMV-SPORT6;
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    0,
                       Score 150; DB 13; Pred. No. 6.4e-33;
    Mismatches
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    240;
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100 TGTGGGCATCGATGTGGGAACAGGTAGTGTCCGTGCGGCTCTAGTGGACCAGAGAGGGCT 159

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                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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National Institutes of Health, Mammalian
Unpublished (1999)
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Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 714)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                 quality sequence start: 7 quality sequence stop: 702
/organism="Mus musculus"
/strain="FVBVN"
/db_xref="taxon:10090"
/clone="IMAGE:5052317"
/clone_lib="NCI_CGAP_Li9"
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256813 MARC 2
BF440790
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                 Design and use of two person discovery in swine Unpublished (2000) Contact: Smith TPL
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                                                                                                                                          1 (bases 1 to 503),
Fahrenkrug, S.C., Fr
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24; Conservative
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/note="organ: liver; Vector: pCMV-SPORT6; Site_1:
Site_2: Sal1; Cloned unidirectionally. Primer: Ol
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 153 c, 219 g 167 t
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                                                                                                                         Freking, B.A., Rohrer, G.A., on, M.P., Grosse, W.M., Benne
Animal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 149.2; DB 13;
Pred. No. 1.1e-32;
0; Mismatches 243;
                                                                                  pooled tissue
  Research
                                                                                                                                                                                                                                                                                                                                    mRNA
5', mRN
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    Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  690
                                                                                  normalized
                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                           Bennett, G.A.,
                                                                                                                                                                                                                                                                                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                Smith, T.P.L.,
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imer: Oligo
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                                                                                      libraries
                                                                                                                         .P.L., Casas,E.
Laegreid,W.W.
                                                                                                                                                                                       Euteleostom1;
Sus.
                                                                                                                                                                                                                                                                                                                                                          EST
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RESULT 13
AI527876
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ORIGIN
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                                                                 DEFINITION
    ACCESSION
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                                                                                                                                                                                                                                    1563 AACAGC 1568
                                                                                                                                                                                                                                                                                                                                                                                                    1443 TGAAAATCGCTGGGATCCAGATTATTTCCGCACCATTGGCCCTTGCAGAGTTAGCGGATGA 1502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 GACTTGCTGGGATAAGGCGGGACATTTCTTTGATCTCCCAGACTTCTTATCGTGGAAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTGATGTCCGTGGAAATGCAGGCGCCGAAGCTTCTGTGGCTCAAAGAGAACTTGAGAGA
                                                                                                                                                                                            CACACC
                                                                                                                                                                                                                                                                                TAATTACAACAAAATAGGAAACAAAGTGCCTGCCTGGAGCTTCTCTTGGAAGTGGGCCT
                                                                                                                                                                                                                                                                                                 AGATTTTATTCGCATTGGTCATCATATTGTTTCTCCCCGGAACCACCTTGTGGAAATGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                AACAGGTGTCCCAGCACGGTCTCTCTGCTCCCTGGTGTGTAAATGGACATACTCAGCA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GA---TCTACGAACGTGCCGGACAATTTTTCGATCTGGCCGATTTTCTGACCTGGCGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PO Box 166, Clay Centry, Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Email: smith@email.marc.usda.gov
Email: smith@email.marc.usda.gov
Email: smith@email.marc.usda.gov
A1527876
676 bp mRNA linear EST 18-MAR-199 unj30c03.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1921444 5' similar to TR:Q04585 Q04585 HYPOTHETICAL 79.2 KD PROTEIN. ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACKWARD: GTTTTCCCAGTCACGACG
Plate: 84 row: G column: 3
Seq primer: ATTTAGGTCACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 \nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -minmatch 12 options.
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/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Sai
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
a 111 c 139 g 124 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sus scrofa"
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Pred. No. 1.5e-32;
0; Mismatches 191;
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REFERENCE
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KEYWORDS
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ORGANISM
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ORIGIN
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Best Local
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1059
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                                                                                                                                                                                                                                                        183 CCTTTTGGCTTTCGCAGAGCAGCCAATTAAGAAGTGGGAGCCTCAATTCAACCACCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      TATTGGTGTTGATGTGGGATCAGGCAGTGTCCGCCCGGGGATTTTTGATCTCAACGGATC
                                                                     TCAAGGGATTGATGCACATCGAATCCGAGGACTTGGTTTTGATGCCACGTGTTCTCTGGT
                                                                                                             GGCAGACGTTTGTGCACAAAGTGTGGCAGGCATCGGTTTTGATGCCACCTGTTCTCTGGT 1118
                                                                                                                                                             GCAGTCCTCAGAGGATATCTGGGCCGCATGCTGCC----TTGTCACAAAGGAAGTTGT
                                                                                                                                                                                       ACAGTCCAGCCAGGAGATCTGGCAGGCGGTCTGTTCATGTATTCGTAATGCGCTCACTCT
                                                                                                                                                                                                                                                                                                                                              TGTGGGCATCGATGTGGGAACAGGTAGTGTCCGTGCGGCTCTAGTGGACCAGAGAGGGCT 182
                                                                                                                                                                                                                                                                                                   TCTGCTATCCCATGCCACAGAAAAAATCACGACTACGCGGCGCAGCGGAAGCCGCGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                           316;
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Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Mėtazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI527876.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: !
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAACCTGCG and 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and clohed into distinct DraIII sites of the pME185-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       performed to exclude fragments <1.5kb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10000"
/clone="IMAGE:1921444"
/clone_lib="Sugano mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was primed with an oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
/lab_host="DH10B"
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Pred. No. 2.8e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           232;
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BASE COUNT
ORIGIN
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R., Collins,F.H., Venter,J.C. and H.
R. Anopheles gambiae EST project
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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45 w. Gude Dr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Contact: Holt R.A.
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Seq primer: M13 Reverse
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1: 2404533151
x: 2404534580
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                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   HoltRA@celera.com
                                                                                                         /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
                                                                                                                                                                                                                                                                                                         /organism="Anopheles
/strain="RSP-ST (Reduchromosome)"
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/clone="19600449631795"
/clone_lib="A.Gam.ad.cDNA1"
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                                                                                           Contact: Robert Strausberg, Ph.D.
Email: Gapabs-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution; MGC clone distribution information can
                                            Unpublished (1999)
                                                                                                                                                                                                                   1 (bases 1 to 983) NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Search completed: March 21, 2003, 23:49:25 Job time: 6112.69 secs
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Best Local Similarity 58.8%;
Matches 267; Conservative
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//tissue_type="large cell carcinoma"
//tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Norgan: lung; Vector: pOTB7; Site_1: XhoI; Sit
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/db_xref="taxon:9606"
/clone="IMAGE:6374458"
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ALIGNMENTS

AAE09779;

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	Staphylococcus epi	cus lacti	Secoisolariciresin	Staphylococcus aur	Staphylococcus aur		Arabidopsis thalia	Arabidopsis thalia		4	Arabidopsis thalia	Secoisolariciresin	Consensus protein	Secoisolariciresin	C	Lactococcus lactis	Short-chain dehydr	Herbicidally activ	Herbicidally activ	Amino acid sequenc	Listeria monocytog	(R)-2-octanol dehy	н	Amino acid sequenc	_	Human polypeptide	Human endocrine po	-	Human secreted pro	Human OXRE-10. Ho	Human PRO238 prote	Human angiogenesis	PR0238 F	Human protein PRO2

WPI; 2001-565596/63. N-PSDB; AAD16811. Positive selection system; metabolise; arabitol; ribitol; mannitol; transgenic cell; marker gene; ribitol dehydrogenase; ribitol kinase, ribitol transporter; rtl operon. Parrott W, 08-MAR-2000; 20000S-0188291. 15-AUG-2000; 20000S-0255595. 08-MAR-2001; 2001WO-US07474 13-SEP-2001. WO200166779-A2 Escherichia coli C. Escherichia coli strain C rtl operon encoding ribitol dehydrogenase 29-NOV-2001 (first entry) (UYGE-) UNIV GEORGIA RES FOUND INC. Lafayette P, Kane Ρ,

Positively selecting transformed cells comprising selectable marker

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RESULT 2
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DT 13-H
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Matches 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene and
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                                                                           08-OCT-1993;
                                                                                                                          08-OCT-1993;
                                                                                                                                                                            09-APR-1995
                                                                                                                                                                                                                                CA2108113-A
                                                                                                                                                                                                                                                                               Streptomyces
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    clavuligerus

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                       (UYAL-) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR77866;
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                                                                                                                                                                                                                                                                                                                                                                                                             Clavulanic acid biosynthesis enzyme; anti
hroad spectrum beta-lactamase inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A 15 kb fragment S. clavuligerus NRRL 5741 genomic DNA (AAO91580), extending downstream from pcbC, included 10 ORFs encoding the enzymes required for clavulinate biosynthesis. ORF8 (oriented in the opposite direction to pcbC) encoded a protein (AAR77866) that showed weak similarity to ribitol 5 PO4 dehydrogenase-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clavulanic acid biosynthesis enzymes and corresp. DNA - useful for biosynthesis of the antibiotic in Streptomyces hosts which do not naturally produce clavulanate

    clavuligerus clavulanic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE07914;
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                                                                                                       15-MAY-2001
                                                                                                                                                       US6232106-B1
                                                                                                                                                                                                                                                             Misc-difference
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91; Conserv
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ilarity 37.3%;
Conservative ''
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Pred. No. 7e-31;
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Best Local
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              24-JUL-1993;
                                                                  02-FEB
                                                                                                                                            Clavulanic acid; antibiotic;
                                                                                                                                                                       Clavulanic
                                                                                                                                                                                                 01-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel enzyme required for clavulanic acid biosynthesis which is useful as broad spectrum beta-lactamase inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD14499, AAD14510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1993;
06-DEC-1995;
                                       15-JUL-1994;
                                                                                          WO9503416-A
                                                                                                                                                                                                                          AAR61477
                                                                                                                                                                                                                                                   AAR61477 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 17; 75pp; English.
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                                                                                                                                                                                                                                                                                                                    240 FIRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 LQLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 MNTPLNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL---GENAYA
                                                                                                                                                                                                                                                                                                                                                                                            VGAVLPGPVVTAL----LDDWPKAKMEEALANGSLMQPIEVAESVLFMVTRSKNVTVRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPSALOGKVALITGASSGIGEATARALAAEGAAVAIAARRVEKLRALGDELTAAGAKVHV
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                                                                                                                                                                                                                                                                                                                                                                    VVVIEPGTTDTELRGHITHTATKEMYEQRISQIRKLQAQDIAEAVRYAVTAPHHATVHEI
                                                                                                                                                                                                                                                                                                                                                                                                                      YMTRAALPHLLRSK-GTVVQMSSIAGRVNVRNAAVYQATKFGVNAFSETLRQEVTERGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LELDVADRQGVDAAVASTVEALGGLDILVNNAGIMLLGPVEDADTTDWTRMIDTNLLGLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SE,
                                                                                                                                                                                                                                                                                                                   243
                                                                                                                                                                       acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 AA;
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                                                                                                                   clavuligerus ATCC 27064
                                                                                                                                                                                               (first entry)
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95US-0567801
              93GB-0015393
                                       94WO-EP02346
                                                                                                                                                                   dehydrogenase sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 366; DB 22;
Pred. No. 7e-31;
1; Mismatches 104;
                                                                                                                                            Augmentin
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RESULT 5
AAY55986
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A new enzyme is disclosed which has clavulanic acid dehydrogenase activity, the enzyme having an apparent mol. wt. of 28 kD (by SDS PAGE) and incorporating the N-terminal sequence PSALOGKYMLITGASSGIGE. The enzyme is derived from the mycelium of a Streptomyces species, especially S. clavuligerus (e.g. ATCC 27064), S. jumojensis (e.g. ATC 2864) or S. katsurahhamanus (e.g. ATCC 27064). The present sequence represents the enzyme from S. clavuligerus ATCC 27064.
                                                                                                                                                                                       gene expression
                                                                                                                                                                                                          Operon; claDH; claR; biosynthetic clavulanate-9-aldehyde reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New clavulanic acid dehydrogenase from Streptomyces, and related DNA and vectors - used to produce beta-lactamase inhibiting clavulanic acid from new 3-oxo:ethylidene analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                         16-JUN-1997;
                                                                                                  01-JUL-1999
                                                                                                                                                             Streptomyces clavuligerus
                                                                                                                                                                                                                                                      S.clavuligerus claDH protein
                                                                                                                                                                                                                                                                                    15-MAR-2000
                                                                                                                                                                                                                                                                                                                 AAY55986;
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             (ANTI ) ANTIBIOTICOS
                                                                      16-JUN-1997;
                                                                                                                               ES2131001-A1
                                                                                                                                                                                                                                                                                                                                           AAY55986 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The enzyme is used to catalyse the biosynthesis of clavulanic acid from a precursor clavulanic acid aldehyde. The obtained clavulanic is in turn a key ingredient in the antibiotic Augmentin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                     VVVIEPGTTDTELRGHITHTATKEMYEQRISQIRKLQAQDIAEAVRYAVTAPHHATVHEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LELDVADRQGVDAAVASTVEALGGLDILVNNAGIMLLGPVEDADTTDWTRMIDTNLLGLM 120
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89; Conserv
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                                                                                                                                                                                                                                                                                  (first entry)
                                           97ES-0001305
                                                                      97ES-0001305
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                                                                                                                                                                                                                                                                                                                                              251
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Pred. No. 4.9e-30;
1; Mismatches 102;
                                                                                                                                                                                                          pathway; clavulanic acid; enzyme;
transcriptional regulator;
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RESULT 6
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QXCCCCCCXXXX77XXR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Improving production of clavulanic acid by Streptomyces super-expression of clar gene.
 N-PSDB;
         WPI; 2002-381255/41
                                                            14-AUG-1997;
08-NOV-1997;
                                                                                                                                        Staphylococcus
                                                                                                                                                                Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                          Doucette-Stamm
                                                                                                      30-APR-2002
                                                                                                                                                         antibacterial;
                                                                                                                                                                                  Staphylococcus
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                                                                                     13-AUG-1998;
                                                                                                                       US6380370-B1
                                                                                                                                                                                                   24-JUL-2002
                                                                                                                                                                                                                   ABP39552;
                                                                                                                                                                                                                                   ABP39552 standard; Protein; 231
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                                           (GENO-) GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                 MPSALQGKVALITGRELGHRRATARALAPEGAAVAIAARRVEKLRALGDELTAAGAKVHV
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DB; AAZ30700.
                                                                                                                                                                                                                                                                              FIRP
                                                                                                                                                                                                                                                                                             VILP
                                                                                                                                                                                                                                                                                                             VVVIEPGTTDTELRGHITHTATKEMYEQRISQIRKLQAQDIAEAVRYAVTAPHHATVHEI
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 ABN92097
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                                                                                                                                                                                                                                                                              247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                  (first
                          LA,
                                           THERAPEUTICS
                                                           97US-055779P.
97US-064964P.
                                                                                     98US-0134001
                                                                                                                                                                                 epidermidis ORF amino acid sequence SEQ ID NO:4397.
                                                                                                                                        epidermidis
                                                                                                                                                                epidermidis;
                                                                                                                                                         therapy
                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.0%;
35.7%;
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Pred. No. 2.7e-28;
0; Mismatches 109
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                                                                                                                                                                 reading
                                                                                                                                                                 frame;
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                                                                                                                                                                 bacterial infection;
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                                                                                                          04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder; gastrointestinal disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.B. The sequence data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            particularly S. epidermidis infections. The sequences screen for compounds able to interfere with the S. epidermidis infection.

N.B. The sequence data for this patent did not form pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic a polypeptide, useful for
                                                                                                                                                                                                                                                                                                 31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          muscular disorder; reproductive disorder; ga-
pulmonary disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB10190 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2001.
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The present invention provides human cDNAs, proteins and related gen DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequise a protein of the invention.
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The present invention relates to the isolation of novel human enzyme C polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences c encoding them. The enzyme polypeptides of the invention may comprise the functional classes of exidoreductases, transferases, hydrolases, lyases, c isomerases or ligases. The sequences of the invention are useful in the c diagnosis, treatment, prevention and/or prognosis of a wide range of exidoredres including hyperproliferative disorders (e.g. cancer), c immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. cancer), c (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), c metabolic disorders (e.g. henylketconuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), c (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis). The blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The c polypucleotides of the invention can also be used in gene therapy.
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24 - FEB - 2000;

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19 - MAY - 2000;

07 - JUN - 2000;

28 - JUN - 2000;

30 - JUN - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrine protein; human; mouse; rabbit; goat; horse; food additive; cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; antinheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; cerebrovascular disorder; breast; liver; cardiovascular disorder; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal; viral infection; ocular disorder; endocrine disorder; dastrointestinal; disorder; cardiovascular disorder; disorder; cardiovascular disorder; fungal infection; viral infection; ocular disorder; endocrine disorder; dastrointestinal; disorder; cardiovascular disorder; dastrointestinal; disorder; cardiovascular disorder; dastrointestinal; disorder; cardiovascular disorder; dastrointestinal; disorder; cardiovascular disorder; dastrointestinal; disorder; cardiovascular disorder; dastrointestinal; disorder; cardiovascular disorder; dastrointestinal; disorder; cardiovascular disorder; dastrointestinal; disorder; cardiovascular disorder; dastrointestinal; disorder; cardiovascular disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestinal; disorder; dastrointestin
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Sequences AAU18282-AAU18507 represent endocrine polypeptides of the invention. Endocrine polypeptides and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by determining the presence or absence of a mutation in an endocrine polynucleotide. The treatable disorders include autoimmune diseases suc
                                                                                                                                                                  Claim
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N-PSDB; AAS29661.
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                                                                                                                                                                                                                                                                                                                                                  Ruben
                                                                                                                                                                604pp;
                                                                                                                                                                                                    treating, preventing and/ or prognosing ne system such as reproductive disorders, so for testing and detection e.g. diagnosis
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07-JUL-2000 11-JUL-2000 11-JUL-2000 11-JUL-2000 14-AUG-2000 11-AUG-2000 11-AUG-2000 11-AUG-2000 11-AUG-2000 11-AUG-2000 11-AUG-2000 11-AUG-2000 11-AUG-2000 11-SEP-2000 11-SEP

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31-JAN-2000;
04-FEB-2000;
19-MAY-2000;
07-JUL-2000;
14-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glomerulonephritis and respiratory disorders such as asthma. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire, wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                     immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulne antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antiinflammatory; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antidiabetic; antimicer; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cerebrovascular disorders such as cerebral ischaemia, nervous system
                                                                                                                          17-JAN-2001;
                                                                                                                                                                                                                                                                                   antiparasitic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM42410 standard;
                                                                                                                                                                                             WO200155449-A1
                                                                                                                                                                                                                                                                 neurological disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis, hyperproliferative disorders such as neoplasms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL------GENA
                                                                                                                                                                                                                              sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRVGAVLPGPV-----VTALLDDWPK-AKMEEALANGSLMQPIEVAESVLFMV-TRSKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLVTFDLIDSGAIVAAAAEILQCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNGGALEELIRELTASHATKVQTHKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEVTVISPGYIHTNLSVNAITADGSRYGVMDTTTAQG---RSPVEVAQDVLAAVGKKKKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVALTKALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YALQLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINA
                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide SEQ ID NO 143
                                                                                                                                                                                                                                                                                                                                                 nootropic; neuroprotective; cytostatic; dermatological; virucide;
uppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
2000US-0179065.
2000US-0180628.
2000US-0205515.
2000US-0216800.
2000US-0218290.
2000US-0225447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                          2001WO-US01346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or liver, cardiovascular disorders such as cardiac arrest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.6%;
                                                                                                                                                                                                                                                                 infection;
                                                                                                                                                                                                                                                                                 immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337
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Pred. No. 8.
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                                                                                                                                                                                                                                                                 nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
3.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107;
                                                                                                                                                                                                                                                                 gene therapy; vaccine
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08-DEC-2000
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06-SEP-2000

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25-SEP-2000

25-SEP-2000

13-OCT-2000

08-NOV-2000

08-NOV-2000

08-NOV-2000

08-NOV-2000

17-NOV-2000

17-NOV-2000

17-NOV-2000

17-NOV-2000
                                                                                                                                                                                                                                                  disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia an epilepsy; and (f) infectious diseases such as viral, bacterial, fung and parasitic infections.
                                                                                                                                                                                                                                                                                                                            and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes meilitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel genes (AAI62752-AAI62961) and proteins (AAM43347-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancer, immune response and neuronal disorde
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen
                                                                         13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL------GENA
                                                                                                                                   Local
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YLVTFDLIDSGAIVAAAAEILQCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFG
                            YALQLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINA
                                                         LRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNGGALEELIRELTASHATKVQTHKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA,
                                                                                                                                                                                                                                       The sequence data
                                                                                                                                   Similarity
                                                                                                                                                                                                                         specification, but was obtained
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN GENOME
                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 143; 532pp + Sequence Listing; English.
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                                                                                                                                                                                337
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2000US-0231243

2000US-0231243

2000US-0234997

2000US-0236476

2000US-0246476

2000US-0246525

2000US-0246526

2000US-0246526

2000US-0246526

2000US-0249211

2000US-0249211

2000US-0249211

2000US-0249211

2000US-0249210

2000US-0250391

2000US-0250391

2000US-0251989

2000US-02511989

2000US-02511989

2000US-02511989

2000US-02511989

2000US-02511989

2000US-02511989
                                                                                                                     Conservative
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                                                                                                                                 24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben
                                                                                                                                                                                                                                      for this patent did not form part of
                                                                                                                   38;
                                                                                                                                Score 311;
Pred. No. 8
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                                                                                                                     Mismatches
                                                                                                                   DB 22;
3.9e-25;
nes 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuronal disorders
                                                                                                                                              Length
                                                                                                                     Indels
                                                                                                                                                                                                                                                                      bacterial, fungal
                                                                                                                                                                                                                           format directly
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                                                                                                                  Gaps
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AFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG

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RESULT 11
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PRO238; PRO364;
PRO840; PRO877;
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Goddard A, Gurney AL,
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18-FEB-2000;
22-FEB-2000;
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26-JUL-1999;
01-SEP-1999;
15-SEP-1999;
         The present invention relates to methods for stimulating or inhibiting angiogenesis and cardiovascularization. The methods involve the use of pharmaceutical compositions based on the following proteins, pR0179, pR0238, PR0364, PR0844, PR0846, PR0160, PR0205, PR0321, PR0332, PR0840, PR0877, PR0878, PR0879, PR0882, PR0885 or PR0887. These proteins were identified by isolating cDNA clones encoding secreted
 proteins were proteins. The
                                                                                  Claim
                                                                                                                diagnose
                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                         Novel PRO
                                                                                                                                               N-PSDB;
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12-MAR-1999;
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                                                                                                                                                                                                                   (GETH
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                                                                                                                                              2000-611444/58
)B; AAA99902.
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                                                                                                                                                                                                                   GENENTECH INC
                                                                                                              O polypeptides and agonists and antagonists of them, used to and treat cardiovascular, endothelial and angiogenic disorders
                                                                                 Fig 4; 181pp; English.
                                                                                                                                                                                                                                      99WO-US1255

99US-014758

99US-0145698

99WO-US20111

99WO-US21090

99WO-US218313

99WO-US28409

99WO-US28565

2000WO-US04342
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 proteins
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                                                                                                                                                                                                                                                                                                                                          99WO-US05028.
99US-0123957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endothelial; angiogenic disorder; PRO179; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO879; PRO882; PRO885; PRO887;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1..21
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the
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 invention
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cDNA clones encoding secreted on may be used to diagnose and
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Paoni NF,
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F. Pitti RM;
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RESULT 12
AAB80238
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15-SEP-1999
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05-CCT-1999
29-NOV-1999
30-NOV-1999
30-NCC-1999
20-DEC-1999
20-DEC-1999
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20-DEC-1999
                                                                                                                                                        07-JUL-1999;
26-JUL-1999;
28-JUL-1999;
                                                                                                                                                                                                                                                                                          antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer; antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal dis
                                                                                                                                                                                                                     18-JAN-2001
                                                                                                                                                                                                                                         WO200104311-A1.
                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                AAB80238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treat cardiovascular, e sequence is one of the
                      (GETH
                                                                                                                                                                                                  22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                            24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    AAB80238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                  ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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5
                                                                                                                                                                                                                                                              sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVRDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEVTVISPGYIHTNLSVNAITADGSRYGVMDTTTAQG--RSPVEVAQDVLAAVGKKKKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRVGAVLPGPV-----VTALLDDWPK-AKMEEALANGSLMQPIEVAESVLFMV-TRSKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVALTKALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YALQLDLFNNQQVDNMLADITELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNGGALEELIRELTASHATKVQTHKP
                     J
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                                                                                                                                                                                                                                                                                                                                     PRO;
                      GENENTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
  ۶
                                                                                                                                                                                                                                                                                  inflammation.
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                                                                                                                                                                                                                                                                                                                                    dermatological; antipsoriatic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242
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                                                                                                                                                                                                                                                                                                                                                       protein.
                                                                                                                                                                                                  2000WO-US04414
                                                                                                                                                                                                                                                                                                                                                                           (first
                                        99WO-US21091
99WO-US21690
99WO-US21547
99WO-US23369
99WO-US28313
99WO-US28313
99WO-US30911
99WO-US30991
99WO-US30991
  Botstein
                                                                                                                                                         99US-0145698
99US-0146222
                                                                                                                                                 99WO-US20594
                                                                                                                                                                              99US-0143048
                      INC.
                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endothelial or angiogenic disorders. The proteins of the invention.
D,
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  Desnoyers
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                    Ą
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 Ĺ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
l.3e-24;
  Eaton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107;
                                                                                                                                                                                                                                                                                            gastrointestinal disorder;
  DĽ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
  Ferrara
                                                                                                                                                                                                                                                                                                                                    antiinflammatory;
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RESULT 13
ABB95441
ID ABB95
XX ABB95
XX ABB95
XX I9-JU
DT 19-JU
DT Human
XX Human
KW Human
KW ather
KW cardi
KW antia
XX antia
XX Homo
XX Homo
XX Homo
XX Homo
XX Homo
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                                                                                                                                                                                                                                                                                                      뭐
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Best Local S
Matches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including the asthmatic acids have applications in molecular biology, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is one of sixty one novel secreted an transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancer squamous cell carcinoma), gastrointestinal disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sixty one nucleic acids encoding PRO polypeptides which are useful the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lunc squamous cell carcinoma) and neurodegenerative diseases (e.g.
                            Homo sapiens
                                                         antiarteriosclerotic.
                                                                       atherosclerosis;
cardiant; cytosta
                                                                                     Human; angiogenesis; PRO atherosclerosis; cardiac
                                                                                                                                 Human angiogenesis related
                                                                                                                                                                                              ABB95441;
                                                                                                                                                                                                                          ABB95441 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's disease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Filvaroff E, Fong S, Gao W, Godowski PJ, Grimaldi CJ, G
Mather JP, Pan J, Paoni NF, Williams PM, Wood WI;
                                                                                                                                                                19-JUL-2002
                                                                                                                                                                                                                                                                                                                                                              215
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                                                                                                                                                                                                                                                                                                                                                                                                                          155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL-----GENA
                                                                                                                                                                                                                                                                                                                                                                                                                                        AFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-081051/09.
DB; AAF72399.
                                                                                                                                                                                                                                                                                                                                 TVRDLV
                                                                                                                                                                                                                                                                                                                                                           IEVTVISPGYIHTNLSVNAITADGSRYGVMDTTTAQG~-RSPVEVAQDVLAAVGKKKKDV
                                                                                                                                                                                                                                                                                                                                                                                      VRVGAVLPGPV-----VTALLDDWPK-AKMEEALANGSLMQPIEVAESVLFMV-TRSKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLVTFDLTDSGAIVAAAAEILQCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YALQLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINA
                                                                                                                                                                                                                                                                                                                                                                                                                     PVALTKALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hybridization probes, and in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 56;
                                                                         cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310
                                                                                                                                                                                                                                                                                                                                 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393pp;
                                                                                                                                                                                                                          Protein;
                                                                    PRO protein; card
diac hypertrophy;
; antiangiogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.4%; Score 309; DB 22; 33.7%; Pred. No. 1.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
                                                                                                                               protein PRO238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
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F, Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerber H,
                                                                                                                                                                                                                          ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                  cardiovascularisation; wound; phy; gene therapy; endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MA,
                                                                      hypotensive; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillan KJ,
Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psoriasis), cancers
                                                                                                                               SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107;
                                                                                                                               NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ME, Godda
Kljavin IC
Tumas D;
                                                                                                                               38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g. Lung
                                                                                    disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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10-MAY-2001;
10-MAY-2001;
25-MAY-2001;
25-MAY-2001;
25-MAY-2001;
30-MAY-2001;
30-MAY-2001;
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25-JUL-2000;
25-JUL-2000;
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28-FEB-
01-MAR-
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20-DEC-
22-JAN-
                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-
08-NOV-
08-NOV-
                   One hundred and eighty seven nucleic acids encoding useful in diagnosis and treatment of cardiovascular infarction), endothelial or angiogenic disorders in
                                                    WPI; 2002-171999/22
N-PSDB; ABL95579.
                                                                          Stephan
                                                                                                                                                                                                            (BAKE/)
(FERR/)
                                                                                                                                                                                                                                                 01-JUN-2001;
20-JUN-2001;
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22-MAR-2001;
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01-DEC-2000
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07-SEP-2000
                                                                                                                         (STEP/)
                                                                                                                                                       (MARS/)
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                                                                                                         (WOOD/)
                                                                                                                                        (PAON/)
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                                                                                          KP,
                                                                                                                                                 GODDARD A.
) GODOWSKI P J.
) GURNEY A L.
) HILLAN K J.
) MARSTERS S A.
) PAN J.
                                                                                                        PAN J.
PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                        -2000
                                                                          i PJ,
JF,
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FERRARA
GERBER H
                                                                                                                                                                                           GERRITSEN M E.
                                                                                          Ferrara N,
                                                                                                                                                                                                                                                 2001US 0866028
2001US 0866034
2001US 0866034
2001US 0870574
2001US 0870574
2001WO US1743
2001WO US1743
2001WO US17800
2001WO US19692
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2000WO-US32678.
2000WO-US32678.
2000WS-0747259.
2000WO-US34956.
2001US-0767609.
2001US-0767609.
2001US-0796498.
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2001US-0802706.
2001US-0808689.
2001US-0816744.
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2000US 0664610.
2000US 0665350.
2000US 242922P.
2000US 2742922P.
2000US 0709238.
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2000WO-US23522.
2000WO-US23328.
2000US+230978P.
                                                                          Watanabe
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2001US
2001US
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                                                                          CK,
                                                                                          Gerber H,
                                                                          Hillan KJ, M
Williams PM,
                                                                                         Gerritsen ME,
                                                                                  Marsters
                                                                          Wood
                                                                          WI,
                                                                                 SA,
                                                                                          Goddard
                                                                          Ye W;
                          PRO polypeptides, (e.g. myocardial
                                                                                 'n,
                                                                                          A
                                                                                  Paoni NF;
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Claim

11;

Fig

38;

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а mammai

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RESULT 14
ABB84835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
 23-JUN-2000;
20-JUL-2000;
25-JUL-2000;
25-JUL-2000;
26-JUL-2000;
02-AUG-2000;
17-AUG-2000;
23-AUG-2000;
07-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
                                                                                                                                                                                                                                                                                                Human; anglogenesis; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; anglogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis;
                                                                                                                                                                                      03-JAN-2002
                                                                                                                                                                                                                  WO200200690-A2
                                                                                                                                                                                                                                                                                                                                                                                                   Human
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                                                                                                                                                                                                                                              HOMO
                                                                                                                                                                                                                                                                       lymphangitis;
wound healing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
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2000US-213637P.
2000US-219556P.
2000US-220624P.
2000US-220664P.
2000WS-220664P.
2000WS-22695P.
2000US-0644657.
2000WS-05233522.
2000WS-US233528.
2000WS-US23358P.
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                                                                                                                                                           2001WO-US19692
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                   tumour anglogenesis; breast carcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 309; DB 23;
Pred. No. 1.3e-24;
8; Mismatches 107
                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                  ID NO:38
                                                                                                                                                                                                                                                                       gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                      liver carcinoma;
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Best Local 9
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                                                                                                                                                                                                                                                                  activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.
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01-DEC-2000

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28-FEB-2001

14-MAR-2001

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31-MAY-2001

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18-SEP-2000;
24-OCT-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One hundred and eighty seven nucleic acids encoding useful in diagnosis and treatment of cardiovascular infarction), endothelial or angiogenic disorders in
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11;
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DB; ABL88090.
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PVALTKALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYE
                            AFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG
                                                                                     YALQLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINA
                                                                                                                      LRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNGGALEELIRELTASHATKVQTHKP
                                                          YLVTFDLTDSGAIVAAAAEILOCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFG
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                                                                                                                                                                                 83; Conser
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JF, Watanabe
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2001US-0767609
2001US-0767609
2001WO-US06520.
2001WO-US06666.
2001US-0808689.
2001US-0816744.
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2001US-0856028.
2001US-0856034.
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2000WO-US32678.
2000US-0747259.
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2000WO-US30952
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2000US-0665350
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L, Hillan KJ, M
CK, |Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                 38;
                                                                                                                                                                                Score 309; DB 23;
Pred. No. 1.3e-24;
8; Mismatches 107;
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M, Wood WI,
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Ye W;
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02-DEC-1998;
10-MAR-1999;
                                            WPI; 200
N-PSDB;
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Hillman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
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Purified polypeptide for treating or preventing disorders associated
                                                                                                                                                                                                                                                                                                                                      06-OCT-1999;
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                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC
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                                              2000-303785/26
)B; AAA09384.
                                                                                                                               JL,
                                                                                                                               Guegler KJ,
JL, Bandman
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                                                                                                                                                                                                                                            98US-0172227.
98US-0155202.
99US-0123911.
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167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
150
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268
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194..2
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/note= "for short-chain dehydogenase"
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/note= "for short-chain dehydogenase"
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O, Azimzai
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Y, Au-Young
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Search completed: March 13, Job time: 22.4884 secs

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Matches 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune/inflammatory disorders (acquired immunodeficiency syndrome (AIDS), asthma, osteoarthritis), and viral infections. The polynucleotides may be used in Southern or Northern analysis, polymerase chain reaction (PCR), or in enzyme-linked immunosorbent assays (ELISA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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83; Conserv
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293
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Pred. No. 1.4e-24;
8; Mismatches 107;
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US-09-134-001C-44397

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US-09-504-358-12

US-09-134-001C-4512

US-09-134-001C-4512

US-09-134-001C-431

US-09-134-001C-5042

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US-09-134-001C-5042

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US-08-793-035-13

US-08-793-035-13

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US-08-793-594-13

US-08-793-594-13

US-08-793-594-13

US-08-940-019-29

US-09-468-738A-29

US-09-448-738A-29

US-09-448-738A-29

US-09-448-738A-3

US-09-344-038A-3

US-09-344-038A-3

US-09-344-038A-3
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1077.057 million cell updates/sec
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4397, Ap
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4512, Ap
2, Appli
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9, Appli
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29, Appli
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US-09-385-028-11
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Patent No. 6232106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Bullding, 400 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DNA Sequence Encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: The Jeni
CITY: Washington
STATE: D.C.
                                                                                                              TYPE:
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INVENTION: Acid Biosynthesis

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Ashish S. Paradkar Kwamena A Aidoo Susan E. Jensen

Enzymes of Clavulanic

45	44	43	42	41	40	39	38	37	36	ω 5	34	ω u	32	31	30	29	28
189	189	189	189	189.5	190	194.5	197.5	197.5	197.5	197.5	198.5	202	202	203	208.5	209.5	214
14.9	14.9	14.9	14.9	15.0	15.0	15.4	15.6	15.6	15.6	15.6	15.7	16.0	16.0	16.0	16.5	16.6	16.9
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327	327	327	301	283	186	255	296	296	292	292	313	256	256	271	243	263	256
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US-08-729-594A-12	US-08-562-114B-12	US-08-375-962B-12	US-09-288-143-98	US-09-134-001C-5346	US-08-858-207A-270	US-08-815-225-4	US-09-940-019-23	US-09-468-738A-23	US-09-940-019-2	US-09-468-738A-2	US-09-413-814-9	US-09-954-314-14	US-09-504-358-14	US-07-637-865-2	US-09-239-052-2	US-09-134-001C-3505	US-08-594-808B-7
Sequence 12, Appl	Sequence 12, Appl	Sequence 12, Appl	Sequence 98, Appl	Sequence 5346, Ap	Sequence 270, App	Sequence 4, Appli	Sequence 23, Appl	Sequence 23, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 9, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 3505, Ap	Sequence 7, Appli

ALIGNMENTS

Application US/09385028

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US-09-385-028-11
Query Match
Best Local Similarity
                                                                                                                                              TELEX: RCA 248593 IDEA UR INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790
APPLICATION NUMBER: US 08/790
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS Price
REGISTRATION NUMBER: 24/514
REFERENCE/DOCKET NUMBER: 1418
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPA
OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                             MOLECULE TYPE:
                                                                                                                                                                                        TELEPHONE: (202)
                                                                                STRANDEDNESS:
TOPOLOGY: lin
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SYSTEM: PC-DOS/MS-DOS
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202) 39305350
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28.9%;
37.3%;
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Score 366; DB 4;
Pred. No. 3.3e-33;
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RESULT 3
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US-09-134-001C-4397
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 GENERAL INFORMATION:
APPLICANT: Rosen et
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                  Sequence 452, Application US/09149476 Patent No. 6420526
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                                                                                                                                                                                                                  LKQSSGHIINLASVSGFEPTKTNAVYGATKAAIHAITQSLEKELARTGVKVTSISPGMVD
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                                                                APPLICATION NUMBER: 60/043,314 FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/047,613
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,582
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,596
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ER APPLICATION NUMBER: 60/043,670
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/056,632
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,664
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,876
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ER APPLICATION NUMBER: 60/056,881
ER APPLICATION NUMBER: 60/056,881
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,881
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R APPLICATION NUMBER: 60/04
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/05
R FILING DATE: 1997-09-05
R APPLICATION NUMBER: 60/05
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R FILING DATE: 1997-08-22
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R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/05
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
                               TVRDLV 242
                                                                                                                                        AFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG
                                                                                                                                                                                                 YALQLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINA
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APPLICATION NUMBER: 60/0
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                                                           IEVTVISPGYIHTNLSVNAITADGSRYGVMDTTTAQG---RSPVEVAQDVLAAVGKKKKDV
                                                                                                                       PVALTKALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYE
                                                                                                                                                                                                                                           LRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNGGALEELIRELTASHATKVQTHKP
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APPLICATION UNMBER: 60/049,
FILING DATE: 1997-06-13
APPLICATION UNMBER: 60/061,
FILING DATE: 1997-10-02
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FILING DATE: 1997-05-
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FILING DATE: 1997-08-22
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83; Conservative
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                                                                                      -VTALLDDWPK-AKMEEALANGSLMQPIEVAESVLFMV-TRSKNV
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                                                                                                                                                                                                                                                                                                    Score 309; DB
Pred. No. 1.5e
38; Mismatches
                                                                                                                                                                                                                                                                                                    DB 4; I
1.5e-26;
nes 107;
                                                                                                                                                                                                                                                                                                                              Length 350;
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R FILING DATE: 1997-08-22
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60/056,903 60/056,637 60/056,882 60/056,872

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APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22

60/056,880

60/056,879 60/056,888

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R APPLICATION NUMBER: 60/05
R FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/0 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22

APPLICATION NUMBER: 60/0 FILING DATE: 1997-05-23

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1997-05-23

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60/056,892

60/056,845 60/056,631

60/057,761

60/047,595

APPLICATION NUMBER: 60/0 FTILING DATE: 1997-08-22

APPLICATION NUMBER: 60/056,864 FILING DATE: 1997-08-22

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APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22

60/056,874 60/056,636 60/056,911 60/056,894

60/056,910

Gaps

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236 214 183 154 123 94 63 EARLIER

APPLICATION NUMBER: 60/0 FILING DATE: 1997-08-22

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; Sequence 4825, Application US/09134001C
; Patent No. 6380370
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US-09-238-481-2
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US-09-134-001C-4825
                                                                                                                                                                                                           US-09-238-481-2
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Huang, Jianzhong
APPLICANT: MCDEVILL, Damien
TITLE OF INVENTION: FabG
FILE REFERENCE: GM10192
                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                             Matches
                                                                                                                                                                                                                                                                                        SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09238481 Patent No. 6110704
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SEQ ID NO 4825
LENGTH: 249
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/238,481 CURRENT FILING DATE: 1999-01-28
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PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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                                                                                                                                                                                                                      ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                    LENGTH: 246
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nes 70; Conserv
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FNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAFRCVRA 130
                                                                            KVAAITGAASGIGLQCAKTLLDAGAKVVLIDREG--DKLHKIVAEL---GENAYALQLDL
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                                        KSALVTGASRGIGRSIALQLAEEGYNVA-VNYAGSKEKAEAVVEEIKAKGVDSFAIQANV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSALVTGASRGIGRSIALQLAEEGYNVA-VNYAGSKDKAEAVVEEIKAKGVESFAIQANV
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                                                                                                                           Conservative
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Pred. No. 1.1e-20;
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Pred. No. 2.4e-21;
                                                                                                                      Mismatches
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                                                                                                                        106;
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RESULT 7
US-09-504-358-12
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                                                            NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09504358 Patent No. 6365376
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 2
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                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                 APPLICANT: Rouviere, Pierre E.
APPLICANT: BIZOSTOWICZ, PATRICIA C.
TITLE OF INVENTION: GENES AND ENZYMES
FILE REFERENCE: BC1001 US NA
                                                                                                                          EARLIER APPLICATION NUMBER: 60/120,70 EARLIER FILING DATE: 1999-February-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/572,810A
CURRENT FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: 09/238,481
PRIOR FILING DATE: 1999-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: FabG
FILE REFERENCE: GM10192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Huang, Jianzhong APPLICANT: McDevitt, Damien
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                        TYPE: PRT
ORGANISM: Brevibacterium sp | HCU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 VLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYGVRVGAVL 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 KVAAITGAASGIGLQCAKTLLDAGAKVVLIDREG--DKLHKIVAEL---GENAYALQLDL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 KSALVTGASRGIGRSIALQLAEEGYNVA-VNYAGSKEKAEAVVEEIKAKGVDSFAIQANV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGFIVSDMTDALSDELKEQMLTQIPLARFGQDTDIANTVAFLASDKAKYIT
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Pred. No. 1.1e-20;
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                                                                                  US-09-134-001C-4512; Sequence 4512, Application US/09134001C; Patent No. 6380370;
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US-09-954-314-12
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 12
LENGTH: 258
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APPLICANT: Rouviere, Pierre E.
APPLICANT: Brzostowicz, Patri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09954314 Patent No. 6465224
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CURRENT FILING DATE: 2001-09-17
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SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/120,702 PRIOR FILING DATE: 1999-February-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES FILE REFERENCE: BC1001 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                      180 SQYGVRVGAVLPG----PVVTALLDDWPKAKME--EALANGSLMQPIEVAESVLFMVTRS 233
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                                                                                                                                                                                                                             181 AKTGVRVNAVAPGYTRTPILEALKAESPETISEWTERIPNGRLNDPSEIADGVVFLMSNA
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                                                                                                                                                                                                                                                                                                                                                                                                           68 DYTNP-----AAVTECAOKLDDEGWPYYGLMANAGIAPSSSAVDYSDELWLRTVDINL 120
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Pred. No. 9.5e-20;
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                                                                                                                                                                   ; TYPE: PRT; ORGANISM: Rhodobacter sphaeroides US-09-287-097-2
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US-09-287-097-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: SCHMUCK, Rainer
APPLICANT: MULLER, Rainer
APPLICANT: WEISSER, Harald
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4512
LENGTH: 263
                                                                                                                                                                                                                                                          SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09287097 Patent No. 6255093
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Best Local
                                                                                                      Query Match
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EARLIER FILING DATE: 1997-04-08
NUMBER OF SEO ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 1999-04-07
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ENGEL, Alfred APPLICANT: KRUGER, Kerstin TITLE OF INVENTION: RECOMBINANT MICROBIAL 3-HYDROXYBUTYRATE DEHYDROGENASE, TITLE OF INVENTION: A PROCESS FOR ITS PRODUCTION AND THE USE THEREOF FILE REFERENCE: 1614-9007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
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                                                                                                                                                                                                                                  LENGTH: 257
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                                         13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVL---IDREGDK--LHKIVAELGENAYALQ 67
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  LNGKRAIVTGSNSGIGLGCAEELARAGAEVVINSFTDRDEDHALAEKIGREHGVSCRYIA 62
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Pred. No. 1.1e-19;
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Pred. No. 9.8e-20;
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TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application Patent No. 5750873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,859
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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221 CELGAHGIRVNCISPFGVATPMLINAWRQGHDASTADDADADIDLDIAVPSDQEVEKMEE
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CITY: W
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                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 333 amino acids TYPE: amino acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                             3 NHSVPSMNTPLNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAELGEN 62
                                                                   RVNALGAALGMKHAALA-MTQRRAGSIISVASVAGVLGGLGPHAYTASKHAIVGLTKNAA
                                                                                                  NLN-INAAFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTR 176
                                                                                                                                       VGFVRCDVSVEEDVERAVERAVARYGRLDVLCNNAGVLGRQTRAAKSILSFDAGEFDRVL
                                                                                                                                                                        AYALQLDLFNNQQVDNMLADIIELAGGLDIFHANAGAY-----IGGPVAEGDPDVWDRVL 117
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                                  RQVSQYGVRVGAVLPGPVVTALL-----
                                                                                                                                                                                                            NGAPTPMPKRLEGKVAIVTGGARGIGEAIVRLFVKHGAKVVIADIDDAAGEALAAALGPH 101
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20037
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77; Conservative
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VENTION: MATERIALS AND METHODS FOR PRODUCING

VENTION: PLANTS WITH SINGLE-SEX FLOWERS
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                                                                                                                                                                                                                                                                                19.4%; Score 245.5; DB 1; 27.5%; Pred. No. 2.1e-19; tive 46; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/440,856A
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                                Indels
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280
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US-09-134-001C-4431
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4431
                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09363189B Patent No. 6242228
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APPLICANT:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
                                                                                                                CURRENT APPLICATION NUMBER: US/09/363,189B
CURRENT FILING DATE: 1990-07-26
PRIOR APPLICATION NUMBER: UP10-216047
PRIOR FILING DATE: 1998-07-30
                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                            APPLICANT: YOKOZEK:
TITLE OF INVENTION:
ORGANISM: Gluconobacter oxydans
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                    TYPE: PRT
                                    LENGTH: 262
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wes 71; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFNNQQVDNMLADIIELAGGLDIFHANAGAYIG-GPVAEGDPDVWDRVLNLNINAAFRCV 128
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                                                                                                                                                                                                                                                SUGIYAMA, MASAKAZU
TONOUCHI, NAOTO
SUZUKI, SHUNICHI
                                                                                                                                                                                            YOKOZEKI, KENZO
VENTION: XYLITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THERE
NCE: 0010-1024-0
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Pred. No. 3.4e-19;
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US-08-793-035-9
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                                   Sequence 9, Application US/08793035 Patent No. 6011201 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5042
LENGTH: 267
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APPLICANT: Lynn Doucette-Stamm et al
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
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 APPLICANT:
                     APPLICANT:
                                                                                                                                                                       187
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                                                                                                                                                                                                                                                                                127 CVRAVLPHMIAQ-RSGDIIFTSSIAGVVPVIWEPI--YTASKFAVQAFVHTTRRQVSQYG 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                      13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVL---IDREGDKLHKI---VAELGENAYAL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 72; Conserv
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                                                                                                                                                                     IRINNISPGAIVT----EHTKEKFSDPTTREETIKMIPAREIGNAQDVANAVLFL 237
                                                                                                                                                                                                                                          GSRETINQFLKENKKGTIINISSVHDTIP--WPNYVHYAASKGGLKLMMETMSMEYAQYG
                                                                                                                                                                                                                                                                                                                       QGDVSIEEDIKRMIETTINHFGTLDIIINNAGFENSIPTHEMSIDDWQKVIDINLTGAFV 128
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Slabas; Antoni R. White, Andrew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.1%; Score 241; DB 4; 30.6%; Pred. No. 4.8e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39; Mismatches 100;
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Search completed: March 13, Job time: 7.82947 secs
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                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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INFORMATION FOR SEQ ID NO: 9:
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APPLICATION NUMBER: US
FILING DATE: 28-JUL-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MCTELECOMMUNICATION INFORMATION: 713.787 1400
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fentem, Phillip A.
TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes
TITLE OF INVENTION: Brassica Napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB95
FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 20-JUL-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                        181
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                                                                                                                                                                          121 INAAFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVS
                                                                                                                                                                                                                   122 GQAITFGGDVSKEADVEAMMKTAIDAWGTIDVVVNNAGITRDTLLIRMKKSQWDEVIDLN
                                                                       242 SRNINVNVVCPGFIASDMTAKLGEDMEKKILGTIPLGRYGQPEDVAGLVEFL 293
                                                                                                                                                                                                                                                                                          66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kammerer, Patricia A. REGISTRATION NUMBER: 29,775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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ZIP: 77210-4433
                                                                                                                                                                                                                                                     61 ENAYALQLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                        QYGVRVGAVLPGPV---VTALLDDWPKAKMEEALANGSLMQPIEVAESVLFM 229
                                                                                                                                            LTGVFLCTQAATKIMMKKRKGRIINIASVVGLIGNIGQANYAAAKAGVIGFSKTAAREGA
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SYSTEM: |PC-DOS/MS-DOS
PatentIn Release #1.0
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                  2003,
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                    16:42:10
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Result
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Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          900:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_EUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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length: 2000000000
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      Match
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US-09-860-670-143
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US-09-907-824-153
US-09-907-824-153
US-09-906-742-153
US-09-906-742-153
US-09-906-838-153
US-09-906-838-153
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US-09-908-859-153
US-09-908-786-153
US-09-908-786-153
US-09-908-786-153
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Sequence 3, Appli
Sequence 143, App
Sequence 153, App
                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09802208B
Publication No. US20030041352A1
GENERAL INFORMATION:
APPLICANT: Parrott, Wayne
APPLICANT: LaFayette, Peter
APPLICANT: Kane, Patrick
APPLICANT: Kane, Patrick
FILE OF INVENTION: Arabitol or Ribitol As Positive Sel
FILE REFERENCE: UGA-855R
CURRENT FILING DATE: 2001-03-08
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                             ; SEQ ID NO 3
LENGTH: 250
; TYPE: PRT
; ORCANISM: Escherichia coli
US-09-802-208B-3
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US-09-802-208B-3
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;	19.1	19.1	19.1	19.1	19.1	19.4	19.5	19.7	19.7	19.8	19.8		19.8				20.2		21.4	22.0	22.3	23.0	24.4	24.4	24.4	24.4
	278	278	278	312	262	253	258	261	266	276	266	266	263	246	246	246	246	272	251	206	203	254	310	310	310	310
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	us-10-033-167-2	US-10-033-223-2	US-10-033-245-2	US-09-885-303A-16	US-09-802-853-6	US-09-815-242-11842	US-09-954-314-12	US-09-815-242-5813	US-09-885-303A-22	US-09-944-160-24	US-09-931-186-18	US-09-981-353-40	US-09-815-242-14092	US-09-815-242-13100	US-09-815-242-12803	US-09-815-242-12123	US-09-815-242-5461	US-09-815-242-12688	US-09-815-242-5689	US-09-997-816-4	US-09-823-901-7	US-09-978-758-2	US-09-909-088B-153	US-09-909-320-153	US-09-903-786-153	US-09-903-749A-153
	2	Sequence 2, Appli	Sequence 2, Appli	Sequence 16, Appl	Sequence 6, Appli	Sequence 11842, A	Sequence 12, Appl	Sequence 5813, Ap	Sequence 22, Appl	Sequence 24, Appl	Sequence 18, Appl	Sequence 40, Appl	Sequence 14092, A	Sequence 13100, A	Sequence 12803, A	•	Sequence 5461, Ap	ς-	e 56	Sequence 4, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 153, App	Sequence 153, App	Sequence 153, App	Sequence 153, App

ALIGNMENTS

Selectable Markers

Best Local Similarity 100.0%; Pred. No. 1.2e-17; Best Local Similarity 100.0%; Pred. No. 1.2e-17; Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 111; 1 MMNHSVPSMNTPLNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAELG 60 1111 11 11 11 11 11 11 11 11 11 11 11 1

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US-09-764-853-498
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Sequence 498, Application US/09764853
Patent NO. US20020090672A1
GENERAL INFORMATION:
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                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 498
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Best Local 9
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                                                                                                    Query Match
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA127P1
CURRENT APPLICATION NUMBER: US/09/860,670
CURRENT FILING DATE: 2001-05-21
                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/764,853 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 289
                                                                                                                                                                         LENGTH: 33
TYPE: PRT
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TYPE: PRT
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                                 13 LNGKVAATTGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL------GENA
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LRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNGGALEELIRELTASHATKVQTHKP 121
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                                                                  Similarity 33.7
83; Conservative
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                                                                                  24.6%;
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                                                                  Score 311; DB 10;
Pred. No. 5.3e-23;
8; Mismatches 107;
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Pred. No. 5.3e-23;
8; Mismatches 107;
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                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
price better Polyperice: 10466-14
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/905,291A CURRENT FILING DATE: 2001-07-12
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APPLICATION NUMBER: PCT/US99/21090 FILING DATE: 1999-09-15 APPLICATION NUMBER: PCT/US99/21547 FILING DATE: 1999-09-15 APPLICATION NUMBER: PCT/US99/23089 FILING DATE: 1999-10-05
                                                                                                                                                                        APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20594
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Williams, P. Mickey
Wood, William, I.
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Mather, Jennie P.
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Grimaldi, Christopher J.
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FILING DATE: 1999-11-30 APPLICATION NUMBER: PCT/US99/28564

APPLICATION

NUMBER: PCT/US99/28313

FILING DATE:

1999-12-02

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Best Local :
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LENGTH: 310
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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                                                              Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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                                                                                                                               Godowski, Paul J.
Grimaldi, Christopher J.
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Filvaroff, Ellen
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Eaton, Dan L.
Roy, Margaret Ann
Stewart, Timothy A.
                               Pan, James
Paoni, Nicholas F.
                                                                                                                                                                Goddard, A.
                                                                                                                                                                               Gerritsen, Mary E.
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; ORGANISM: Homo
US-09-902-853-153
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Best Local
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CURRENT FILING DATE: 2001-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/143,048 PRIOR FILING DATE: 1999-07-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                         237 TVRDLV 242
                                                                                                                                                                         155
                                                                                                                                                                                                                124 AFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG
                                                                                                                                                                                                                                                                                                                                                                           13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL------GENA
                                                                                                                                                                                                                                                                                         64 YALQLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINA 123
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FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US00/00219 FILING DATE: 2000-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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APPLICATION NUMBER: PCT/US99/28565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US99/23089 FILING DATE: 1999-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/146,222 FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/145,698 FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US99/30911 FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US99/28564
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                                                                                                                             VRVGAVLPGPV--+--VTALLDDWPK-AKMEEALANGSLMQPIEVAESVLFMV-TRSKNV
                                                                                                                                                                         PVALTKALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYE
                                                                                                                                                                                                                                                                                                                                                     LRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNGGALEELIRELTASHATKVQTHKP
                                                                                  IEVTVISPGYIHTNLSVNAITADGSRYGVMDTTTAQG---RSPVEVAQDVLAAVGKKKKDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.48;
Similarity 33.78;
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278
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 309; DB 9;
Pred. No. 7.4e-23;
8; Mismatches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                            107;
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RESULT 6
US-09-907-824-153
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                   OR APPLICATION NUMBER: PCT/US99/28565
OR FILING DATE: 1999-12-02
OR APPLICATION NUMBER: PCT/US99/30095
OR FILING DATE: 1999-12-16
OR APPLICATION NUMBER: PCT/US99/30911
OR FILING DATE: 1999-12-20
OR APPLICATION NUMBER: PCT/US99/30999
APPLICATION NUMBER: PCT/US00/00219 FILING DATE: 2000-01-05
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/21547
APPLICATION NUMBER: PCT/US99/21547
APPLICATE: 1999-09-15
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FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
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FILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/28564
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FILING DATE: 1999-10-05
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Mather, Jennie P.
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Grimaldi, Christopher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fong,
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Filvaroff, Ellen
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b. US20020197671A1
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RESULT 7
US-09-907-841-153
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US/60/143,048
PRIOR APPLICATION NUMBER: US/60/145,698
PRIOR APPLICATION NUMBER: US/60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US/60/146,222
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Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
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LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                    FILE REFERENCE: 10466-14 CURRENT ADDITION: Acids Encoding the Same
                                                                                                                                                                             APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRVGAVLPGPV----VTALLDDWPK-AKMEEALANGSLMQPIEVAESVLFMV-TRSKNV
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Grimaidi, Christopher J
Gurney, Austin L!
Hillan, Kenneth, J.
Kijavin, Ivar J.
                                                                                                                                                                                                                                                                             Roy, Margaret Ann
Stewart, Timothy A.
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Gerber, Hanspeter
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Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 309; DB 9;
Pred. No. 7.4e-23;
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; ORGANISM: Homo sapiens
US-09-907-841-153
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 153
LENGTH: 310
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 153, Application US/09904011 Publication No. US20030003530A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 YALQLDLFUNQQVDUMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL------GENA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 LRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNGGALEELIRELTASHATKVQTHKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
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APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
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                                                                                Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
                                                            Kljavin, Ivar J.
Mather, Jennie P.
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Botstein, David
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                 Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                               Goddard, A.
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Filvaroff, Ellen
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                                                  Pan, James
                                                                                                                                                                               Gerritsen, Mary E
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Pred. No. 7.4e-23;
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; ORGANISM: Homo US-09-904-011-153
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PRIOR FILING DATE: 1999-09-15
PRIOR PRIOR DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PPLICATION NUMBER: PCT/US99/23089
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-07-07
PRIOR PPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-08
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PRIOR FILING DATE: 1999-09-08
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PRIOR FILING DATE: 1999-09-13
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CURRENT FILING DATE: 2001-07-11
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237 TVRDLV
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APPLICATION NUMBER: PCT/US00/00219
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FILING DATE: 1999-12-16
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                                                                             IEVTVISPGY I HTNLSVNAITADGSRYGVMDTTTAQG--RSPVEVAQDVLAAVGKKKKDV
                                                                                                                                                                                      PVALTKALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYE
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33.7%; Pred. No. 7.4e-23;
tive 38; Mismatches 107
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US-09-906-742-153; Sequence 153; A
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CURRENT FILING DATE: 2001-07-16
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PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
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                                APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
                                                                                                                                                                                                           FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
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APPLICATION
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FILING DATE: 1999-12-16
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Stewart, Timothy A.
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Grimaldi, Christopher J.
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5. US20030023054A1
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US-09-906-742-153
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 153
LENGTH: 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 153, A Publication No.
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Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                  APPLICANT:
                                                                                     CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
                                                                                                                                   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE PETERBENCE: 10466-14
               PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
                                                                                                                          FILE REFERENCE: 10466-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 LRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNGGALEELIRELTASHATKVOTHKP 94
APPLICATION NUMBER: US 60/143,048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG 183
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                                                                                                                                                                               Williams, P. Mickey Wood, William, I.
                                                                                                                                                                                                                               Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                     Tumas,
                                                                                                                                                                                                                                                                                                           Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                               Gurney, Austin L.
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Grimaldi, Christopher J.
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Ferrara, Napoleone
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Botstein, David
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                                                                                                                                                                                                                                                                         Paoni,
                                                                                                                                                                                                                                                                                            Pan, James
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                                                                                                                                                                                                                   Daniel
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APPLICATION NUMBER: PCT/US99/20594 FILING DATE: 1999-09-08

APPLICATION NUMBER: US FILING DATE: 1999-07-28

1999-07-28

60/146,222 60/145,698

APPLICATION NUMBER: US FILING DATE: 1999-07-26

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                                                                                                                                                                  US-09-907-613-153
                                                                                                                                                                                        RESULT 11
                                                                                                        GENERAL INFORMATION
                                                                                                                       Sequence 153, Application US/09907613 Publication No. US20030027145A1
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                 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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TYPE: PRT
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es 83; Conserv
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Eaton, Dan L.
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Pred. No. 7.4e-23;
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LRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNGGALEELIRELTASHATKVQTHKP LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL------GENA 63 Matches

Conservative

38;

Mismatches

107;

Indels

18;

Gaps

5

13 35

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; TYPE: PRT; ORGANISM: Homo sapiens US-09-907-613-153
                                                                                                                            NUMBER OF SEQ ID
SEQ ID NO 153
   Query Match
Best Local
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APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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CURRENT FILING DATE: 2001-07-17
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                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/143,048 FILING DATE: 1999-07-07 APPLICATION NUMBER: US 60/145,698 FILING DATE: 1999-07-26
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                                                                                                                                                                                  APPLICATION NUMBER: PCT/US00/00219
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FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/28565
                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
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 Similarity
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Cao, Wei-Qiang
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Stewart, Timothy A.
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Mather, Jennie P.
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24.48;
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 Score 309; DB 9;
Pred. No. 7.4e-23;
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CURRENT APPLICATION NUMBER: US/09/907,942
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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US-09-907-942-153
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APPLICANT: Genentech, Inc.

Ashkenazi, Avi
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                            OR FILING DATE: 1999-07-28
OR APPLICATION NUMBER: PCT/US99/20594
OR FILING DATE: 1999-09-08
OR FILING DATE: 1999-09-13
OR APPLICATION NUMBER: PCT/US99/2094
OR FILING DATE: 1999-09-15
OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/21547
OR APPLICATION NUMBER: PCT/US99/21547
OR APPLICATION NUMBER: PCT/US99/23089
OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/23089
OR FILING DATE: 1999-10-05
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APPLICATION NUMBER: PCT/US99/28214 FILING DATE: 1999-11-29
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Botstein, David
Desnoyers, Luc
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Mather, Jennie P.
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Stewart, Timothy A.
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Kljavin, Ivar J.
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Grimaldi, Christopher
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Best Local S
Matches 83
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SEQ ID NO 153
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PRIOR FILING DATE: 1999-12-02 |
PRIOR APPLICATION NUMBER: PCT/US99/30095
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Ashkenazi, Avi
Roy, Margaret Ann
Stewart, Timothy|A.
                                                                          Kljavin,
                                                                             Gurney, Austin L:
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher
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Goddard, A.
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Botstein, David
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                                                            Mather, Jennie P
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                               Nicholas
                                                                                                                                                                                                                           Sherman
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33.7%; Pred. No. 7.4e-23;
Live 38; Mismatches 107
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LENGTH: 310
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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PRIOR FILING DATE: 1999-09-08
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237 TVRDLV 242
                                                                                      184 VRVGAVLPGPV-----VTALLDDWPK-AKMEEALANGSLMQPIEVAESVLFMV-TRSKNV 236
                                                                                                                                                                               124 AFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG
                                                                                                                                                                                                                                                                 64 YALQLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINA 123
                                                                                                                                                                                                                                                                                                                      35 LRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNGGALEELIRELTASHATKVQTHKP 94
                                                                                                                                                                                                                                                                                                                                                13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL-----GENA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
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                                        IEVTVISPGYIHTNLSVNAITADGSRYGVMDTTTAQG---RSPVEVAQDVLAAVGKKKKDV
                                                                                                                                    PVALTKALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYE
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RESULT 14
US-09-904-859-153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Secréted and Transmembrane Polypeptides and Nucleic FILTE OF INVENTION: Acids Encoding the Same FILE REFERNCE: 10466-14, CURRENT APPLICATION NUMBER: US/09/904.859 CURRENT FILING DATE: 2001-07-12 PRIOR APPLICATION NUMBER: US/655,350 PRIOR FILING DATE: 2000-09-18 PRIOR APPLICATION NUMBER: PCT/US00/04414 PRIOR APPLICATION NUMBER: US/09-10-2-22 PRIOR FILING DATE: 2000-02-22 PRIOR FILING DATE: 2000-02-22 PRIOR FILING DATE: 2000-01-2-22 PRIOR FILING DATE: 105-07-07 PRIOR FILING DATE: 105-07-07 PRIOR FILING DATE: 1999-07-07
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FILING DATE: 1999-11-129
APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/23089
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FILING DATE: 1999-09-13
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                                                                             APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
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                     FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US00/00219
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Grimaldi, Christopher J
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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Mather, Jennie P.
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; PRIOR FILING DATE: 2000-01-05; NUMBER OF SEQ ID NOS: 423; SEQ ID NO 153; LENGTH: 310; TYPE: PRT; ORGANISM: Homo Sapien US-09-904-859-153.
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US-09-909-204-153
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            CURRENT APPLICATION NUMBER: US/09/909,204
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
                                                                                                   APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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APPLICATION NUMBER: US 60/145,698
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Roy, Margaret Ann
Stewart, Timothy A.
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Grimaldi, Christopher J.
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Eaton, Dan L.
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Ashkenazi, Avi
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Best Local
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LENGTH: 310
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                                   237 TVRDLV 242
                                                                                                       184 VRVGAVLPGPV-----VTALLDDWPK-AKMEEALANGSLMQPIEVAESVLFMV-TRSKNV
                                                                                                                                                                                                                                         64 YALQLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINA 123
                                                                                                                                                                                                                                                                                        35 LRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNGGALEELIRELTASHATKVQTHKP
                                                                                                                                                                                                                                                                                                                          13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL------GENA
                                                                                                                                                                                                                                                                                                                                                              Local Similarity es 83; Conserv
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APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US99/30095 FILING DATE: 1999-12-16
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APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/21547
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                                                                     IEVTVISPGYIHTNLSVNAITADGSRYGVMDTTTAQG--RSPVEVAQDVLAAVGKKKKDV
                                                                                                                                                                  AFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG 183
                                                                                                                                           PVALTKALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYE
                                                                                                                                                                                                                   YLVTFDLTDSGAIVAAAAEILQCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFG
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Pred. No. 7.4e-23;
B; Mismatches 107;
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Maximum Match 100%
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Db 1 MKHSVSSMNTSLSGKVAAITGAASGIGLECARTILGAGAKVVLIDREGEKLNKLVAELGE Db 1 MKHSVSSMNTSLSGKVAAITGAASGIGLECARTILGAGAKVVLIDREGEKLNKLVAELGE Oy 62 NAYALQLDLENNQQVDNMLADITELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNI Db 61 NAFALQVDLMQADQVDNLLQGILQLTGRLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNI OY 122 NAAFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQ OY 122 NAAFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQ OY 121 NAAFRCVRSVLPHLIAQKSGDIIFTAVIAGKVPVIWEPIYTASKFAVQAFVHTTRRQVSQ OY 122 YGVRVGAVLPGPVVTALLDDWPKAKMEEALANGSLMQPIEVAESVLFMVTRSKNVTVRDL OD 181 YGVRVGAVLPGPVVTALLDDWPKAKMEEALANGSLMQPIEVAESVLFMVTRSKNVTVRDL OV 182 YGVRVGAVLPGPVVTALLDDWPKAKMEEALANGSLMQPIEVAESVLFMVTRSKNVTVRDL OV 11 YGVRVGAVLPGPVVTALLDDWPKAKMDEALADGSLMQPIEVAESVLFMVTRSKNVTVRDL OY 242 VILPGSVDL 250 OY 11 III OY 241 VILPGSVDL 249	CD DEBEE OCHU PEROCHU OCHI	30 277 21.9 251 2 AH2042 31 275.5 21.6 260 2 H70758 32 273.5 21.5 260 2 H70758 33 272.5 21.5 266 2 F83127 35 271.5 21.5 266 2 F83127 36 271 21.4 238 1 D69930 37 270 21.3 249 2 B97605 38 270 21.3 249 2 B97605 39 269 21.3 249 2 AB1886 40 268.5 21.2 248 2 F82128 41 268.5 21.2 248 2 F82128 42 268.5 21.2 248 2 F82128 43 267 21.1 258 2 H64122 43 267 21.1 258 2 H75616 44 267 21.1 278 2 E83152 45 266.5 21.1 244 2 T12051
REGURLHALIVALIGE OL 	pro pro he	3-oxoacyl-[acyl-ca acetoin dehydrogen probable fab63 proc hypothetical prote probable short-cha oxidoreductase [improbable 3-oxoacyl cyclohexanol dehydr hypothetical prote 3-oxoacyl-(acyl-ca probable 3-oxoacyl acyl-ca probable 3-oxoacyl ydfg protein - Hae oxidoreductase, sh probable short-cha 3-oxoacyl-[acyl-ca short-cha 3-oxoacyl-[acyl-ca short-cha short-cha short-cha short-cha 3-oxoacyl-[acyl-ca

RESULT 2

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A; Nolecule type: DNA
A; Residues: 1-242 <KUR>
A; Cross-references: GB: AE008918; PIDN: AAL54222.1;
A; Cross-references: Strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Contents: annotation
A;Contents: annotation
A;Note: Cys-30 and Cys-126 are carboxymethylcysteine
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
C;Keywords: oxidoreductase
F;15-189/Domain: short-chain alcohol dehydrogenase homology <SADH>
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ribitol 2-dehydrogenase (EC 1.1.1.56) -
C:Species: Enterobacter aerogenes
C:Date: 13-Jul-1981 #sequence_revision 1
C:Accession: A94585; A00344
R;Hartley, B.S.
                                                                      A;Map position: II
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the Atlas, June A; Reference number: A94585 A; Accession: A94585
                                                                                                                           A; Gene: BMEII0980
                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                               A;Reference number: AD3252;
A;Accession: AC3632
                                                                                                                                                                                                                                                            A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Reference number: AD3252; PMID:11756688
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A; Residues: 1-247 <HAR>
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                   Loca 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VILPNSVDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAYALQLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNI 121
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                  Similarity
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                  66.68;
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 36;
                Score 843; DB 2;
Pred. No. 1.1e-62;
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Pred. No. 9.3e-82;
3; Mismatches 14
   Mismatches
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 44;
                                                                                                                                                                          PID:g17985193; GSPDB:GN00191
                                  Length 242;
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A;Map position: linear chromosome C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology C;Keywords: oxidoreductase |
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B98199
ribitol 2-dehydrogenase (EC1.1.1.56) [imported] -
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001
C:Accession: B98199
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C; Genetics:
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A; Residues: 1-243 <KUR>
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46.18;
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Pred. No. 3.1e-40;
2; Mismatches 78;
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RESULT 5
AG3087
ribitol 2-dehydrogenase rdh [imported] C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11

11-Jan-2002

Agrobacterium tumefaciens (strain C58,

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K; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C., Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizoblum mellilot A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: E95283
                                                                  A;Molecule type: DNA
A;Residues: 1-249 <KUDA
A;Residues: 1-249 <KUDA
A;Residues: 1-249 <KUDA
A;Residues: 1-249 <KUDA
A;Cross-references: GB:AE006469; PIDN:AAK64831.1; PID:g14523244; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
B; Chain, P.; Cowie, A.; Davis, R.W.; Dreamo, S.; Federspiel, N.A.; Fisher
C; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; I
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.;
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21366234; PMID:11474104
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E95283
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A;Title: The Genome of the Natural Genetic
A;Reference number: AB2577; PMID:11743193
A;Accession: AG3087
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Contents: annotation C;Genetics: A;Gene: SMa0320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSym2
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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8 (Dupont)
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Pred. No. 3.1e-40;
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                                                                                                                                                                                                                           Abola, P.; Ampe, F.; Barloy-Hubler S.; Federspiel, N.A.; Fisher, R.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:BA000018; PID:g13702428; A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-231 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G90050
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQ-YGVR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAFR 126
  SPGMVDTAITAAYNPSDRKK
                                        LPGPVVTALLDDWPKAKMEEALANGSLMQPIEVAESVLFMVTRSKNVTVRDLVILP
                                                                              AALPTMLEQSSGHLINTASISGFEVTKSSTIYSATKAAVHTITQGLEKELAKTGVKVTSI
                                                                                                            AVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYGVRVGAV 189
                                                                                                                                                          VTNKEEVDELMKIAQQTFGGLDIVINSAGQMLSSKITDYQVDEWDSMIDVNIKGTLYTAQ
                                                                                                                                                                                                 LFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAFRCVR
                                                                                                                                                                                                                                       TYLTDKIAVYTGAGSGIGEAIATLLHEEGAKVYLAGRNKDKLQNVANQLAQDSVKVVPTD
                                                                                                                                                                                                                                                                           TPLNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAELGENAY-ALQLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGAVLPGPVVTALLDDWP----KAKMEEALANGSLMQPIEVAESVLFMVTRSKNVTVRDL 241
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75; Conserv
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                                                                                                                                                                                                                                                                                                                 26.2%; Score 331; DB 2; 31.8%; Pred. No. 3.6e-20; tive 54; Mismatches 99;
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; Pred. No. 2.7e-20;
45; Mismatches 105
- LDPQDIAEAVLYALTQPKHVNVNEITVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:BAB43569.1;
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Sekimizu,
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RESULT T17307

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hypothetical protein DKF2p5660084.1 - human

(:Species: Homo saplens (man)

(:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T17307

R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemasubmitted to the Protein Sequence Database, September 1999

A;Reference number: Z18724

A;Accession: T17307

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-325 <BLO>
A;Cross-references: EMBL:AL117567
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                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-255 <FAR>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, March A;Description: Hereditary instability of (A;Reference number: Z22886
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Haloferax volcanii
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000
C;Accession: T44991
R;Farahani, R.; Imbeault, J.C.; St Jean, A.; Chan, C.C.Y.; Allard, G.; Char.
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                                                                                                                                                                                                   A; Note: expressed during heat shock C_i; Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oxidoreductase [imported] - Haloferax volcanii megaplasmid pHV3
C; Species: Haloferax volcanii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                          A; Map position: megaplasmid pHV3
                                                                                                                                                                                                                                                                                                                                                                      A;Status:
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                                                                                           13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL---GENAYALQLD
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                                                       LDGKVAIVTGASSGIGSATAKSLASRGASVVVAARREGELEELAATIEDDGGDALVVPTD
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                                                                                                                                 72;
                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Imbeault, J.C.; St Jean, A.; Chan, C.C.Y.; Allard, G.; Charlebois,
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                strain
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33.3%;
                                                                                                                                                23.4%; Score 295.5; DB: 30.0%; Pred. No. 3.6e-17
                                                                                                                                                                                                                                                                                                DS2
                                                                                                                                 57;
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Pred. No. 9.7e-18;
                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          megaplasmid
                                                                                                                                                                   DB 2;
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                                                                                                                                 Indels
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C;Becies: Listeria innocua
C;Bate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #tex
C;Accession: AD1489
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.;
R;Glaser, P.; Frangeul, G.; Duchaud, E.; Durand, L.; Dussı
                                                                                                                                                                                                                                                                                                                                     RESULT
AD1489
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: B39930
A; Molecule type: DNA
A; Residues: 1-248 <GI
A; Cross-references: (
                                                                         ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1489
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
F;6-187/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 65, 1127-1141, 1991
A;Title: Entry of Listeria monocytogenes into cells is mediated A;Reference number: A39930; MUID:91292517; PMID:1905979
A;Accession: B39930
                                                      A; Status: preliminary
                                                                                                                                                          A; Authors: Kreft, J.; Kuhn, M.;
                                                                                                                                                                          D.; Jones, L.M.; Karst, Science 294, 849-852, 2
                                                                                                                                                                                                                                                                                                                 oxidoreductase homolog lin0452 [imported] - Listeria innocua
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A; Residues: 1-248 <GAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAVLPGPVVTALLDDWPKAKMEEALANGSL-----MQPIEVAESVLFMVTRSKNVTVRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAVLPSFIAQKSGHIIATSSVAGLKAYPGGAVYGATKWAVRDLMEVLRMESAQEGTNIRT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG--VRV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKNKVIIITGASSGIGKATALLLAEKGAKLVLAARRVEKLEKIVQIIKANSGEAIFA-KT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVTKREDNKKLVELAIERYGKVDAIFLNAGIMPNSPLSALKEDEWEQMIDINIKGVLNGI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAFRCV 128
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79; Conserv
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                    <GLA>
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GB: AL592022;
                                                                                                                                                                                                                                                                            #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
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                                                                                                                                      Kunst, F.; Kurapkat,
N.; Tierrez, A.; Vazqı
  PIDN:CAC95684.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gouin, E.;
                                                                                                                                    pkat, G.; Madueno,
Vazquez-Boland, J.
PID:g16412893;
                                                                                                                                                                                                                     Dussurget,
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                                                                                                                                                                                                                   Baquero, F.; Bercl
urget, O.; Entian,
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    GSPDB:GN00178
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tian, K.D.;
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                                                                                                                                        Voss, H.; W
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Fsihi,
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J.

242 240 TVGPTS

VILPGS

245 247

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A; Experi
C; Geneti
A; Gene:
C; Superf
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Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.; A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxidoreductase homolog lmo0432 [imported] - Listeria monocytogenes (strain EGD-e
C;Specises: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AI1128
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; F
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A;Gene: lmo0432
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-248 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 AAVLPSFIAQKSGHIIATSSVAGLKAYPGGAVYGATKWAVRDLMEVLRMESAQEGTNIRT 181
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                                                                                                                                                                                                                                                                                                                             13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIV----AELGENAYALQL 68
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIV----AELGENAYALQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVTKREDNKKLVELAIERYGKVDAIFLNAGIMPNSPLSALKEDEWEQMIDINIKGVLNGI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAVLPGPVVTALLDDWPKAKMEEALAN-----GSLMQPIEVAESVLFMVTRSKNVTVRDL
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VTIYPAAINTELLETITDKETEQGMT---SLYKQYGITPDRIASIVAYAIDQPEDVNVNEF
                                            GAVLPGPVVTALLDDWPKAKMEEALANGSL----MQPIEVAESVLFMVTRSKNVTVRDL
                                                                                        AAVLPSFIAQKSGHIIATSSVAGLKAYPGGAVYGATKWAVRDLMEVLRMESAQEGTNIRT
                                                                                                                                       RAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG--VRV
                                                                                                                                                                                      DVTKREDNKKLVELAIERYGKVDAIFLNAGIMPNSPLSALKEDEWEQMIDINIKGVLNGI 121
                                                                                                                                                                                                                                  DLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAFRCV 128
                                                                                                                                                                                                                                                                              Similarity
77; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 292; DB 2;
Pred. No. 6.8e-17;
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Pred. No. '
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                                                                                                                                                                                                                                                                                                                                                                              Mismatches 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 248
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                                                                                                                                                                                                                                                                                                                                                                            Indels 14;
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                                                                                           181
                                            241
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Fsihi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wehland
                                                                                                              A; Title: DNA Sequence of both chromosomes of the cholera A; Reference number: A82035; MUID:20406833; PMID:10952301 A; Accession: B82181
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              A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-252 <HEI>A;Cross-references: GB:AE004236;
                                                                                                                                                                                 R;Heldelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers l, R.R.; Mekalanos, J.J.; Vehter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                              oxidoreductase, short-chain dehydrogenase/reductase family VC1591 [imported] C;Specles: Vibrio cholerae C;Deceles: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 03-Aug-2001 C;Accession: B82181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                         B82181
A; Experimental source:
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vaguez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
AG1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: fabG
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
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                                                                                                                                                                                                                                                                   Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: AG1672
DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-247 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: AG1672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.; Jones,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-ketoacyl-acyl carrier prótein reductase homolog fabG [imported] - Listéria
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243
                                            245
                                                                                        183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                            PGSV
                                                                                        VAPGFITTEMTDKLDDKTKEAMLAQIPLGAYGTTEDIANAVLFLASDASKYITGQTLSVD 242
                                                                                                                                  VLPGPVVTAL---LDDWPKAKMEEALANGSLMQPIEVAESVLFMVT-RSKNVTVRDLVIL 244
                                                                                                                                                                                                           RAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYGVRVGA 188
                                                                                                                                                                                                                                                                        NVAIAEDVDAFFKQAIERFGRIDILVNNAGITRDNLLMRMKEDEWDDVININLKGTFLCT
                                                                                                                                                                                                                                                                                                                                                              LQGKVAVVTGGSRGIGRDIAIKLAKEGANIFFNYNGSPEAAEETAKLVAEHGVEVEAMKA
GGMV
                                                                                                                                                                                 KAVSRTMMKQRAGKIINMASVVGLIGNAGQANYVASKAGVIGLTKTTARELAPRGINVNA
                                                                                                                                                                                                                                                                                                                  DLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAFRCV
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246
                                            248
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.8%; Score 289; DB 2; 32.4%; Pred. No. 1.2e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g16414422; GSPDB:GN00178
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Voss, H.; Wehla
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Fsihi,
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serogroup

GB:AE003852; NID:g9656095; PIDN:AAF94745.1; O1; strain N16961; biotype El Tor

GSPDB:GN

pathogen

Vibrio cholerae

Vibrio

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J. Bacteriol. 178, 3275-3284, 1996
A;Title: Ti plasmid-encoded genes responsible for catabolism of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine many control of the crown gall opine control opine many control opine many control opine many control opine many control opine many control opine many control opine many control opine many control opine many control opine many control opine many control opine many control opine many control opine many control opine many control opine many control opine many control opine many control opine many c
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: oxidoreductase
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A;Experimental source: strain 15955
C;Genetics:
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A; Reference number: 222872; MUID: 96236046; PMID: 8655509

A; Accession: T44932
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A; Residues: 1-248 <KIM>
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Best Local 9
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                                                                                                                                                                                                                                                190 LPGPVVTALLDDWPKAKMEEALANGSLMQPIEVAESVLFMVTRSKNVTV-----RDLV 242
                                                                                                                                                                                                                                                                                                                                                           123
                                                                                                                                                                                                                                                                                                                                                                                                                         130 AVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYGVRVGAV 189
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237 PLPGS 241
                                                                                    243 ILPGS 247
                                                                                                                                                                         183 CPGAVDTQQRSD-----NHVDDRSQLLQPEDVAEYIAFIVTRHDRVYIGEVSPIAQQLK 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAE---LGENAYALQLD 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 VQHKSEVDALAKAAFERFGAVDILVNNAGVAIHNTIPNIKEADWDWMMAINLKGTFLCTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 LFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAFRCVR 129
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Local Similarity 33.5%; Pred. No. 1.5e-16;
es 82; Conservative 30; Mismatches 117; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LQGKTAVITGAGRGIGRATALELAKEGCNVVLAAIELNEVEAVAEEVRAIGSEALALRTD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LTHKVALVTGAANGIGLAIAERLYQEGATLALADWNEEQL-AIVIEQFDSARVYAQKVDV 62
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                                                                                                                                                                                                                                                                                                                                             AFFQHMCDRRHGHIINVVSRARKVASAKFGAYAASKFGMLGFTQTTDQEGIEFGVKATAV 182
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Search completed: March 13, 2003, 16:55:58 Job time: 9.69205 secs

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   SwissProt_40:*
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     GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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LINX_PSEPA
YK02_MYCTU
YOKD_BACSU
FABG_VIBHA
DHAA_BACSU
FABG_VIBHA
DHAB_BACSU
FABG_AQUAE
FAG1_SYNY3
HDHA_CLOSO
UCPA_SALTY
YDFG_ECOLI
PABG_CUPL
ACT3_STRCO
Y41A_ACHISN
BDHA_RHIME
ACT3_STRCO
Y41A_ACHISN
BDHA_BACSU
Y16A_BCSU
Y16A_BCSU
Y16A_BCSU
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UCP
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p00335 klebsiella
Q92ek7 listeria mo
p25145 listeria mo
p251481 bacillus su
Q9x248 thermotoga
p50198 pseudomonas
Q10855 mycobacteri
p14802 bacillus su
Q9kqh7 vibrio chol
p45200 haemophilus
p55336 vibrio harv
p3971 bacillus su
O67610 aquifex aeo
p73574 synechocyst
p59200 clostridium
p37441 salmonella
p39831 escherichia
p14634 streptomyce
p5541 rhizobium m
p16544 streptomyce
p5541 rhizobium s
Q9x6u2 alcaligenes
p40864 salmonella
p28643 cuphea lanc
Q56318 thermotoga
p39440 bacillus su
Q11020 mycobacteri
p37440 escherichia
Q8xbj4 escherichia
Q8xbj4 escherichia
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Q8xbj4 escherichia
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mycobacteri

bacillus su

vibrio chol

haemophilus

vibrio harv

bacillus su

bacillus su

aquifex aeo

4 synechocyst

clostridium

salmonella

escherichia
                                                                                                                                                                                                  homo sapien
rhizobium m
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2-dehydrogenase la aerogenes. ; Proteobacteri la. lin_28451; iD=28451; and D; 86050423; pubMe 86050424; pubMe dehydrogenase es of wild-type J. 230:569-578 FROM N.A. 86050424; pubMe Nortonepase es of wild-type J. 230:579-585 J. 230:79-585 J.	STP (Rel. (Rel. (Rel.	18.7 18.3 18.3 18.2 18.2 11.0 11.9 17.9 17.9
2-dehydrogenase (EC) 11a aerogenes. a; Proteobacteria; gan 11a. A, and D; A, and D; A, and D; A, and D; B6650423; pubMed=3904 1. dehydrogenase of Kic ies of wild-type and n J. 230:569-578(1985) T. NOTTON P.M. Hartl 1 dehydrogenase of Kic ral gene. ". J. 230:579-585(1985) E FROM N.A. "86520424; pubMed=2931 T. NOTTON P.M. Hartl 1 dehydrogenase of Kic ral gene. ". J. 230:579-585(1985) ALVTIC ACTIVITY: Ribit ACTOR: BINDS THE COEN UNIT: HOMOTETRAMER. CELLANEOUS; THE SEQUEN ILANITY: BELONGS TO TH R) FAMILY ILANITY: BELONGS TO TH R) FAMILY 11 dend this statement is requires a license a an email to license el an email to license el an email to license el 34418; SO7135. 7135; S07135.	STANDARD; STANDARD; 1. 01, Cre 1. 08, Las 1. 40, Las	- 2255 2554 2556 2456 2566 2561 2561 2561
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Best Local
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between the
                                                                                              Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Darwar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget (
Entlan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell
Narguez-Boland J.-A., Voss H., Wehland J., Cossart P.;
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CLIP 11262 / Serovar 6a;
MEDLINE-21537279; PubMed-11679669;
                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002
15-JUN-2002
15-JUN-2002
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VARIANT
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Y452_LISIN
                                                               "Vazquez-Boland J.-A., Voss H., Wehland J., C.
"Comparative genomics of Listeria species.";
Science 294:849-852(2001)
-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN D
                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                             Hypothetical LIN0452.
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PS00061; ADH_SHORT;
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CARBOXYMETHYLATION
CARBOXYMETHYLATION
CARBOXYMETHYLATION
A -> P (IN STRAIN-D)
AV -> SS (IN REF. 2)
AV -> D (IN REF. 1)
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Pred. No. 2e-8
0; Mismatches
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                                                                SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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15-JUN-2002
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STRAIN-EGD-e / Serovar 1/2a;

MEDLINB-21537279; PubMed-11679669;

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Bloekker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget

Entian K.-D., Fsihi H., Garcia-del Porttillo F., Garrido P.,

Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
                                                                                                                                                                                                                                                                                                                                                                     Y432_LISMO
P25145;
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PROSITE; PS00061; ADH_SHORT; 1.
Hypothetical protein; Oxidoredum
NP_BIND 9 31 NAI
ACT_SITE 154 154
BY
SEQUENCE 248 AA; 26808 MW;
                                                                                                                                                      Cell 65:1127-1141(1991).
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                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                              repeat
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                                                                                                                                                                                                                   MEDLINE=91292517; PubMed=1905979;
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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al oxidoreductase )
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Pred. No. 4.1e-17;
8; Mismatches 105;
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BY SIMILARITY
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-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Burchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Chamings N.J., Daniel R.A.,
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RA Choi S.K., Codani J.J., Connerton I.F., Chamings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Chiller R.D., Capita N., Fulli R., Calleron N.,
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RA Guiseppi G., Guy B.,J., Haga K., Haicch J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kuita K., Lapidus A., Cardinois S., Lauber J., Lazarevic V.,
RA Kuita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kuita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Naizuno M., Moesti D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Soeffone F.,
RA Schiguchi A., Tacconi E., Takasqi T., Takahashi H., Takemaru K.,
RA Viari A., Wandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wandenbol M., Vannier F., Vassarotti A.,
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Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]
NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
-i- PATHWAY: FIRST, REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
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"Bacillus subtilis acyl carrier protein
lipid biosynthesis genes",
J. Bacteriol. 178:4794-4800(1996).
                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed
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STRAIN-MSB8 / DSM 3109;

MEDICINE-9287316; PubMed=10360571;

MELSON K.E. Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Linher K.D., Ketchum K.A.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

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Nature 399:323-329(1999).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Pfam; PF00106; adh_short; 1.
PRINTS; PR000080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
NADP; Com
Fatty acid biosynthesis; Oxidoreductase; NADP; Com
Fatty acid biosynthesis; Oxidoreductase; NADP; Com
Fatty acid biosynthesis; Oxidoreductase; NADP; Com
Fatty acid biosynthesis; Oxidoreductase; NADP; Com
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-oxoacyl-[acyl-carrier protein] reductase (E
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7; Mismatches 1
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Best Local S
Matches 75
                                                                Nagata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;
"Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol
dehydrogenase gene involved in the degradation of gamma-
hexachlorocyclohexane in Pseudomonas paucimobilis.";

J. Bacteriol. 176:3117-3125(1994).

-i- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL
(2,5-DDOL) INTO 2,5-DICHLOROPTONOUINONE (2,5-DCHQ). LINX IS NOT
ESSENTIAL TO GAMMA-HCH DEGRADATION.

-i- PATHWAY: DEGRADATION OF GAMMA-HEXACHLOROCYCLOHEXANE.
                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase
(2,5-DDOL dehydrogenase).
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P50198;
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Bacteria; Proteobacteria;
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NP_BIND 10 34 NADP (BY SIMILARITY).
ACT_SITE 154 154 BY SIMILARITY.
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PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
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or send an email to license@isb-sib.ch).
                                                                        MEDLINE-98295987; pubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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  1551 / Oshkosh;
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25492 MW;
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Pred. No. 5.
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8C52703FF76382CF CRC64;
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Best Local :
                                                                                              P14802;
01-APR-1990
01-DEC-1992
16-OCT-2001
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EMBL; AE007057;
HSSP; P19992; 11
TIGR; MT2058; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Oxidored NP_BIND 11 35 N NP_ACT_SITE 153 153 CONFLICT 174 174 SECUENCE 260 AA; 27030 MW;
                       Bacillus subtilis.
Bacteria; Firmicutes;
RCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains.";
Submitted (APR-2001) to
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                                                                     Hypothetical YOXD.
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InterPro; IPR002198; ADH_short.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
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SEQUENCE FROM
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European Bioinformatics Institute. There are no
by non-profit institutions as long as its co
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1 oxidoreductase yoxD (EC)
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Best Local
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Ahn K.S., Wake R.G.;
"Variations and coding fe
                                                                           FABG_VIBCH

Q9KQH7;

16-OCT-2001

16-OCT-2001

16-OCT-2001
                                    acyl carrier |
FABG OR VC202
                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat)
3-oxoacyl-[acyl-carrier protein] reductase
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SubtiList; BG11048; yoxD.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                          Vibrio
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PROSITE; PS00061; ADH_SHORT; 1.

Hypothetical protein; Oxidoreductase;
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EMBL; Z99114; CAB13743.1;
PIR; S01270; S01270.
HSSP; O70351; 1E3S.
NCBI_TaxID=666;
           Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                  LQHKTALITGGGRGIGRATALALAKEGVNIGLIGRTSANVEKVAEEVKALGVKAAFAAAD
                         cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
           Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155
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                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                   protein
                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haarsma
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155 B
; 25299 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1849493;
                                                                                                                                                                                                   -SIELNLTDGNPEKVMQPEDLAE---YMVAQLK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                     21.4%; Score 271; DB 1 32.5%; Pred. No. 3e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            features of
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           gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eductase; Complete proteome.
NAD OR NADP (BY SIMILARITY).
BY SIMILARITY.
', 9CC7A8D1204DF248 CRC64;
                                                                                                                                   PRT;
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           subdivision;
                                                              reductase (E
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           Vibrionaceae;
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                                                              (3-ketoacyl
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Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=El Tor N16961 / Serotype O1;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C
                                                     P45200;
01-NOV-1995
01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit.
Haemophilus influenzae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00080; SDRFAMILY. PROSITE; PS00061; ADH_SHORT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE004276; AAF
HSSP; P19992; 1HDC.
TIGR; VC2021; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement
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SEQUENCE FROM N.A.
STRAIN=El Tor N16961 /
                             HI1430.
                                          Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002198; ADH_
Pfam; PF00106; adh_short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- CATALYTIC ACTIVITY: ((3R)-3-hydroxyacyl-[acyl-carrier NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
-1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cholerae
                                                                                                                YDFG_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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                                                                                                                                                                                                                                             RGMMKKRQGRIINVGSVVGTMGNAGQANYAAAKAGVIGFTKSMAREVASRGVTVNTVAPG
                                                                                                                                                                                                                                                                                                   PESIEAVLKAITDEFGGVDILVNNAGITRDNLLMRMKEEEWSDIMETNLTSIFRLSKAVL
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an email to license@isb-sib.ch).
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5 (Rel. 32, Last se
2 (Rel. 41, Last an
al oxidoreductase H
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                                                                                                               STANDARD;
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1; 25566
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                                                                                    Created)
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 gamma
                                       sequence update) annotation update HI1430 (EC 1.-.
                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                               Score 268.5; DB 1;
Pred. No. 4.9e-15;
9; Mismatches 107;
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BY SIMILARITY
                                                                                                                  PRT;
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J.с.,
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RESULT 11
FABG_VIBHA
ID FABG_V
AC P55336
DT 01-CCT
DT 01-CCT
DT 01-CCT
DT 02-CCT
DC 03-OXOO
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HSSP; P50162;
TIGR; H11430;
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ACT_SITE
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MEDLINE-95350630, PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                             P55336;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
3-oxocyl-[acyl-carrier protein] reductase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for cor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 269:496-512(1995).
Science 269:496-512(1995).
--- STMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
   Vibrio harveyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Oxidoreductase; Complete proteome.
NP_BIND 7 31 NAD OR NADP (BY SIMILARITY).
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PROSITE; PS00061; ADH_SHORT; 1.
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                                 carrier protein
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252 AA;
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                                                                                DHBA_BACSU STANDARD,

101-FEB-1995 (Rel. 31, Created)

11-NOV-1995 (Rel. 32, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
ACT_SITE
                                                        Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                              BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002198; ADH_
Pfam; PF00106; adh_short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation of Vibrio harveyi acyl carrier protein and the fabG, and fabF genes involved in fatty acid biosynthesis.";

J. Bacteriol. 178:571-573(1996).

-i- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]

NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.

-i- PATHWAY: FIRST | REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation of Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00080; SDRFAMILY. PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U39441; AAC43589.1; HSSP; P19992; 1HDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                          NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96134997; PubMed-8550484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                          183
                                                                                                                                                                                                                                                                                                     193
                                                                                                                                                                                                                                                                                                                                   123
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                                                                                                                                                                                                                                                                                                                                                                                               63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SDR) FAMILY.
                                                                                                                                                                                                                                                                       FIETDMTKALNDDQRAATLSNVPA-GRLGDPREIASAVVFLAS
                                                                                                                                                                                                                                                                                                                                                                                             VESIEATLKTINDECGAIDILVNNAGITRDNLLMRMKDDEWNDIINTNLTPIYRMSKAVL
                                                                                                                                                                                                                                                                                                   PVVT----ALLDDWPKAKMEEALANGSLMQPIEVAESVLFMVT
                                                                                                                                                                                                                                                                                                                                 RGMMKKRAGRIINVGSVVGTMGNAGQTNYAAAKAGVIGFTKSMAREVASRGVTVNTVAPG
                                                                                                                                                                                                                                                                                                                                                               PHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYGVRVGAVLPG
                                                                                                                                                                                                                                                                                                                                                                                                                          NQQVDNMLADTIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAFRCVRAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEGKIALVTGASRGIGRAIAELLVERGATVIGTATSEGGAAAISEYLGENGKGLALNVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid biosynthesis; Oxidoreductase; NADP.

acid biosynthesis; Oxidoreductase; NADP.

NADP (BY SIMILARITY).

NADP (BY SIMILARITY).

BY SIMILARITY.

NCE 244 AA; 25519 MW; FC41A1C65B8CDAAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.1%; Score 266.5; DB 1; 32.3%; Pred. No. 7.2e-15; tive 39; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH_short.
                                                          Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma subdivision;
                                                          Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrionaceae;
                                                                                                                    OE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrio.
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STRAIN-168 SEQUENCE FROM N.

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Best Local
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EMBL; L08644; AAA18899.2; -
EMBL; 299120; CAB15190.1; -
PIR; PN0683; PN0683.1; -
HSSP; P08074; ICYD.
                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene
                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; 1.
Oxidoreductase; NAD; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Graumann P.L., Schmid R., Marahiel M.A.;
Submitted (OCT-1997) to the SWISS-PROT data bank.
-I- CATALYTIC ACTIVITY: 2,3-dihydro-2,3-dihydroxybenzoate
2,3-dihydroxybenzoate + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 133:119-121(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97080557; PubMed-8921902;
Rowland B.M., Grossman T.H., Osburne M.S., Taber H.W.;
"Sequence and genetic organization of a Bacillus subtilis
encoding 2,3-dihydroxybenzoate biosynthetic enzymes.";
Gene 178:119-123(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia
                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SubtiList; BG11019; dhbA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94040785; PubMed=8224884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and mapping of the Bacillus Escherichia coli ent genes.";
                                        186
                                                                                               126
                                                                                                                         130
                                                                   190
                                                                                                                                                     66
                                                                                                                                                                                                                       70
                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: 2,3-dihydroxybenzoate biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic.
INDUCTION: IN RESPONSE TO LOW TEMPERATURE.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
              VTVRDLVILPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SDR) FAMILY.
                                                                                                            AVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYGVRVGAV
<del>--</del>
                                       SPGSTETDMQWSLWADENGAEQVIKGSLETFKTGIPLKKLAKPSDIADAVLFLVSGQAGH
                                                                                                                                                  VRDSAAIDEITARIEREMGPIDILVNVAGVLRPGLIHSLSDEEWEATFSVNSTGVFNASR
                                                                                                                                                                                                      IEGKIAFITGAAQGIGEAVARTLASQGAHIAAVDYNPEKLEKVVSSLKAEARHAEAFPAD
                                                                LPGPVVTAL-LDDWPKAKMEEALANGS------LMQPIEVAESVLFMVT-RSKN
                                                                                            SVSKYMMDRRSGSIVTVGSNPAGVPRTSMAAYASSKAAAVMFTKCLGLELAEYNIRCNIV
                                                                                                                                                                           LFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAFRCVR
                                                                                                                                                                                                                                                                          Similarity
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157
146
231
247
261 AA;
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37
157
6 234
256
27494 MW;
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                                                                                                                                                                                                                                                             48;
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BY SIMILARITY.
P -> D (IN REF. 2).
IADA -> MRC (IN REF. 2).
TMHNLCVDGG -> RCIFMRRCAT (
                                                                                                                                                                                                                                                                          Score 264.5; DB 1
Pred. No. 1.1e-14;
                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                 00B0EFBA53AB407C CRC64;
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                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                             115;
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                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
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Best Local S
Matches 67
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98196666; PubMed-9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Auj-
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 067610;
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acyl carrier protein FABG OR AO_1716
                                                                                                                                                                                                                                                                                                                PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000752; AAC07575.1; -. HSSP; P50163; 2AE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Aquificae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-oxoacyl-(acyl-carrier protein) reductase (EC
                                                                                                                                                                                                                                                                                                    Fatty acid
                                                                                                                                                                                                                                                                                                                                           Pfam; PF00106; adh_short;
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002198; ADH_short.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FABG_AQUAE
 176
                                                   116
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                         180
                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SDR) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITMHNLCVDGGA
 APRNVLVNAVAPGFIETDMTAVLSEEIKQKYKEQIPLGRFGSPEEVANVVLFLCSELASY
                                                                            NINAAFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQV
                                                                                                       GVEMNLLSEESINKAFEEIYNLVDGIDILVNNAGITRDKLFLRMSLLD-----WEEVLKV
                                                                                                                                                         MEIKLQGKVSLVTGSTRGIGRAIAEKLASAGSTVIITGTSGERAKAVAEEIANKYGVKAH
                                                                                                                                                                                  MNTPLNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL---
                         SQYGVRVGAVLPGPV---VTALLDDWPKAKMEEALANGSLMQPIEVAESVLFMVTRSKNV
                                                   NLTGTFLVTQNSLRKMIKQRWGRIVNISSVVGFTGNVGQVNYSTTKAGLIGFTKSLAKEL
                                                                                                                               ALQLDLFNNQQVDNMLADIIELAGGLDIFHANAG----AYIGGPVAEGDPDVWDRVLNL
                                                                                                                                                                                                            . Similarity 67; Conserv
                                                                                                                                                                                                                                                                                       biosynthesis; Oxidoreductase; NADP; Complete 12 36 NADP (BY SIMILARITY)
                                                                                                                                                                                                                                                             12
157
248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                 36
157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37, (Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257
                                                                                                                                                                                                                                                             26867, MW;
                                                                                                                                                                                                                         20.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aquificae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reductase).
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                                                                                                                                                                                                             56;
                                                                                                                                                                                                          Score 262.5;
Pred. No. 1.6e
56; Mismatches
                                                                                                                                                                                                                                                             NADP (BY SIMILARITY).
BY SIMILARITY.
; 5CFD9EB9AD83F2C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (class);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248
                                                                                                                                                                                                          1.6e-14;
ches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aquificales;
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bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1.1.100) (3-ketoacyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .G., Lenox
Aujay M.,
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aquificaceae;
                                                                                                                                                                                                                                                                                                   proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aquifex
                                                                                                                                                                                                                                      248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huber R.,
                                                                                                                                                                                                             17;
                                                                                                                                                                                   -GENAY
                                                                                                                                                                                                             Gaps
                                                                                                                                                           60
 235
                                                                                                       115
                                                    175
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Qγ . .

237

TVRDLVILPGSV 248

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions." DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Miyajima N., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechocystis sp. (strain PCC 6803)
Bacteria; Cyanobacteria; Chroococca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00080; SDRFAMILY. PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D90907; BAA17614.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fatty acid biosynthesis; Oxidoreductase; NADP; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FABG1 OR SLR0886.
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                                                                                                                                                                                                                                                                                                                       11 TPLNGKVAAITGAASGIGLQCAKTLLDAGAKVVL-IDREGDKLHKIVAEL---GENAYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH. PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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GAVLPGPVVTALLDDWPKAKMEEALANGSLMQPIEVAESVLFMVT 231
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                                                           CTKAVSKLMLKQKSGRIINITSVAGMMGNPGQANYSAAKAGVIGFTKTVAKELASRGVTV
                                                                                                              CVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYGVRV
                                                                                                                                                                       QANVANADEVDQLIKTTLDKFSRIDVLVNNAGITRDTLLLRMKLEDWQAVIDLNLTGVFL
                                                                                                                                                                                                                                QLDLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAFR 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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247 AA;
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Pred.
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BY SIMILARITY.
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No. 4.4e-14;
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HDHA_CLOSO
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Matches 72
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ACT_SITE
SEQUENCE
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01-OCT-1996 (Rel. 34, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L12058; AAA53556.1; -. HSSP; P25529; 1AHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restues by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydroxysteroid dehydrogenase gene from Clostridium sordellii.";

J. Bacteriol. 176:4865-4874(1994).

-:- CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-

cholanate + NADP(+) = 3-alpha,12-alpha-dihydroxy-7-oxo-5-beta-

cholanate + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium sordellii.
Bacteria; Firmicutes; Clostridia;
                                                                                                                                                                                                                                                                                                                                                 PROSITE; PRO0061; ADH_SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coleman J.P., Hudson L.L., Adams M.J.; "Characterization and regulation of the NADP-linked 7 alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94327451; PubMed=8050999
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INDUCTION: BY BILE ACID. EXPRESSED DURING GROWTH-PHASE.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SDR) FAMILY.
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                                                                                                                                                                          LENKVALVTSATRGIGLASAIKLAQNGAIVYMGVRRLEATQEICDKYKEEGLILKPVFFD
RCNAVLPGLIATDAAMNSMPDEFRKSFLSHVPLN-RIGNPEDIANSVLFFV
                            RVGAVLPGPVVT----ALLDDWPKAKMEEALANGSLMQPIEVAESVLFMV
                                                                                   FRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYGV
                                                        YRLSKLIIPHMIENKGGSIVNISSYGGSIPDISRIGYGYSKSGVNNITKQIAIQYAKYGI
                                                                                                                                           NQQVD----NMLADIIELAGGLDIFHANAGAYIGGP-----VAEGDPDVWDRVLNLNINAA
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7; Mismatches
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No. 1e-13;
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BY SIMILARITY.
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(EC 1.1.1.159) (Bile
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Search completed: March 13, 2003, 16:53:42 Job time : 6.96689 secs

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Result
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Copyright (c) 1993 - 2003
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Q99rf5 staphylococ
Q9rh22 zymomonas m
Q9bf6 homo sapien
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034187
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ALIGNMENTS

RESULT 1 Q9F4L7

Q9F4L7 Q9F4L7;

PRELIMINARY;

PRT;

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01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21,

Created)
Last sequence update)
Last annotation update)

Bacteria; Proteobacteria;

gamma subdivision; Enterobacteriaceae;

NCBI_TaxID=562; Escherichia Escherichia coli;

RTLD

Ribitol dehydrogenase.

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Best Local Similarity
Matches 250; Conserv
                                                                                         PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
Oxidoreductase.
SEQUENCE 250 AA; 26693 MW; 1787D4CE
                                                                                                                          InterPro; IPR002198; ADH_short. Pfam; PF00106; adh_short; 1. PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                             "A non-antibiotic marker for amplification of plant transformation vectors in E. coli.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                            EMBL; AY005817; AAG01883.1; -. HSSP; 070351; 1E6W.
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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(SDR) FAMILY
                                             Conservative
                                                                                           26693 MW; 1787D4CEBFD6C6DE CRC64;
                                             100.0%; Score 1265; DB 2; 100.0%; Pred. No. 6e-91; tive 0; Mismatches 0;
                                                                   DB 2; Length 250;
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XX MEDIXINE-20020109; PubMed-11756688;

XA MEDIXINE-20020109; PubMed-11756688;

XA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

XA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

XA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

XA Haselkorn R., Kyrpides N., Overbeek R.;

YI' The genome sequence of the facultative intracellular pathogen

YI' The genome sequence of the facultative intracellular pathogen

YI' Brucella melitensis.";

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01-MAR-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
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SEQUENCE 242 AA;
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PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
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Brucellaceae; Brucella.
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Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo I Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning, J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo Zhang S., Yoo H., Tao Yi, Biddle P., Jung M., Krespan W., Perry Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Mester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the plant pathogen Agrobacterium tumefactens C58."; Science 294:2323-2328(2001). EMBL; AE009360; AAL45117.1; ---
EMBL; AE008252; AAK89116.1; ---
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RDH OR ATU4323 OR AGR_L_1076.
Agrobacterium tumefaciens (strain C58 / ATCC
Bacteria; Proteobacteria; alpha subdivision;
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Paradkar A.S., Aidoo K.A., Jensen S.E.;
"A pathway-specific transcriptional activator regulates late
"A valanic acid biosynthesis in Streptomyces clavuligerus.";
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Paradkar A.S., Aidoo K.A., Wong A., Jensen S.E.;
Paradkar analysis of a beta-lactam resistance gene encoded within the cephamycin gene cluster of Streptomyces clavuligerus.";
J. Bacteriol. 178:6266-6274(1996).
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Jensen S.E., Elder K.J., Aidoo K.A., Paradkar A.S.
"Enzymes catalyzing the early steps of clavulanic
are encoded by two sets of paralogous genes in Str
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MEDLINE-98267213; [PubMed-9602162;

Perez-Redondo R., Rodriguez-Garcia A., Martin J.F., Liras P.;

Perez-Redondo R., Rodriguez-Garcia A.
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01-JUN-2001
01-JUN-2001
01-JUN-2002
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Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
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                                                                                                                                                             SPECIES-S.aureus (strain Mu50), an MEDLINE-21311952; PubMed-11418146;
                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical protein SAV2478.
SAV2478 OR SA2266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q99RF5
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=382;
                                                                                                                                                                                                                                                                     NCBI_TaxID=158878, 158879;
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249 AA; 26553 MW; ODFE1F7597361F5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244
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Pred. No. 2.8e-18;
5; Mismatches 105
                                                                                                                                                                                      and S.aureus
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                                                                                                                                                                                                                                                                                                                   group;
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Ito T.,
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RESULT
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pfam; pF00106; adh_short; 1.
PRINTS; PR000080; SDRFAMILY.
Oxidoreductase; Hypothetical protein; Complete proteome.
SEQUENCE 231 AA; 24578 MW; EED1BCE261E87778 CRC64;
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Lancet 357:1225-1240(2001).
                                                                                                                                                                              Oxidoreductase. SEQUENCE 248
                                                                                                                                                                                                                                                InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY
                                                                                                                                                                                                                                                                                                               (SDR) FAMILY.
EMBL; AF088897; AAI
HSSP; P14061; 1FDS
                                                                                                                                                                                                                                                                                                                                                                                    containing rrnA operon."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENAS!
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Bacteria; Proteobacteria; alpha
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of 65G3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ZM4;
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MNQNIRNKIVVITGASSGLGAETARHLSDLGATVVLGARREERIATLANSIVAK-GGQAL
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                                        MNTPLNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKL----HKIVAELGENAY
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l Similarity 31.8%;
75; Conservative 5
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77; Conserv
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                                                                                       Conservative
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                                                                                  25.1%; Sc
31.6%; Pr
tive 53;
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of meticillin-resistant Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          cosmid clone of Zymomonas mobilis
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                                                                                                         Score 317; DB 2
Pred. No. 5e-17;
                                                                                                                                                                                                                           UNKNOWN_1
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Pred. No. 3.7e-18;
4; Mismatches 99;
                                                                                                                                                                                1C8335777C5E1EB1 CRC64;
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                                                                                       Mismatches
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Best Local S
Matches 83
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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EMBL; BC009679; AAH09679.1; -.
EMBL; BC009679; AAH09679.1; -.
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Submitted (JUN-2001) to the
-!- SIMILARITY: BELONGS TO
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Mammalia; Eutheria;
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                                                                                                                                       AFRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG
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                                                  IEVTVISPGYIHTNLSVNAITADGSRYGVMDTTTAQG--RSPVEVAQDVLAAVGKKKKDV
                                                                                                                    PVALTKALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYE
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Primates;
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33.7%; Pred. No. 3e-16;
Live 38; Mismatches 1
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Query Match
                                                                                     O92NF8 PRELIMINARY; PRT; 253 AA.
092NF8; O1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
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"Towards a Catalog of Human Genes and Proteins: Sequencing ar Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
Genome Res. 11:422-435(2001).
Putative oxidoredúctase protein.
R02247 OR SMC01635.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobácteria; alpha subdivision;
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Pfam; PF00106; adh_short;
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EMBL; AL117567; CAB55997.1;
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01-MAY-2000
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STRAIN-ATCC 14706;

MEDLINE-20145393; PubMed-10681342;

Patel R., Piper K.E., Cockerill F.R., Steckelberg J.M., Yous

"The blopesticide Paenibacillus popilliae has a vancomycin r

gene cluster homologous to the enterococcal VanA vancomycin
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01-OCT-2000 (TrEMBLrel. 15, Last sequence upda
01-DEC-2001 (TrEMBLrel. 19, Last annotation upda
01-DEC-2001 (TrEMBLrel. 19, Last annotation upda
Hypothetical 26.4 kDa protein
Paenibacillus popilliae (Bacillus popilliae).
Bacteria; Firmicutes; Bacillus/Clostridium gr
Pfam;
                                            EMBL;
HSSP;
                                                                                                                                                             gene
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                                                                                                              Antimicrob. Agents Chemother.
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NCBI_TaxID=382;
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P14061; 1FDS.
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PF00106;
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253 AA;
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Last sequence update)
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Best Local
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01-MAR-2001
01-JUN-2002
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacterineae; Nocardiaceae; Rhodo
                                                                                                                                                                                                                                                                            Oxidoreductase. SEQUENCE 246
                                                                                                                                                                                                                                                                                                                                               Pfam; PF00106; adh_short; PRINTS; PR00080; SDRFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         App1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van der Vlugt-Bergmans C.J.B., van der Werf M.J.;

"Genetic and biochemical characterization of a novel monoterpene epsilon-lactone hydrolase from Rhodococcus erythropolis DCL14.";

Appl. Environ. Microbiol. 67:733-741(2001).
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PROSITE; PS00061; ADH_SHÖRT; UNKNOWN_1.

Hypothetical protein; Oxidoreductase.

SEQUENCE 248 AA; 26432 MW; A122A9FD7799B10C CRC64;
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                                                                                                                                                                                                                                                                                                                       PROSITE; PS00061; ADH_SHORT; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002198; ADH_short.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21091964; PubMed-11157238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDR-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239
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61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL----GENAYALQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                            (SDR) FAMILY.
DVARVEDAERMVETAVAHFGGLDIAVNNAG---VGVPVKASVGDTGFEEWRRVLDVNLDGA
                                                                                                              MNTPLNGKVAAITGAASGIGLQĆAKTLLDAGAKVVLIDREGDKLHKIVAELGENAVALQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTIGPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVVNPDDSQQLVQLAKDTF---GGVDVIFLNAGLMPNSPLSELKTDEWNSMVDVNIKGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLFN---NQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IENKVVVITGASSGIGEATAKLLAEKGAKVVLGARREEHLVKLVEEIKSNGGQAAYRV-T
                                                                                   MSYALEGKVAVVTGGGSGIGAACVRQLCALGASVVVADIVFDNATLVAKEFGDRAVAVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVILPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRTATIYPAAINTELLGTITDKNISEGMTALYEQYGISPDRVANIVAFAIDQPEDTNVNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRVGAVLPGPVVTALLDDWPKAKMEE---ALANGSLMQPIEVAESVLFMVTRSKNVTVRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG--
                                           DLFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPV--AEGDP--DVWDRVLNLNINAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
83; Conser
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                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                         2AE1
                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                              25058 MW;
                                                                                                                                                                                                      23.4%;
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16,
21,
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 298; DB
Pred. No. 1.5e
13; Mismatches
                                                                                                                                                                                                      Score 295.5; DB 2; Pred. No. 2.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                              6DEC1B36FE9AA34A CRC64;
                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                 246;
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                                                                                                                                                                                 Gaps
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                                             124
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RESULT 15
Q9EXG3
ID Q9EXG
AC Q9EXG
DT 01-MA
DT 01-MA
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Best Local :
Q9EXG3;
Q9EXG3;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pHV3.
Archaea; Euryarchaeota; Halc
Halobacteriaceae; Haloferax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    034187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Hereditary instability of the megaplasmid pHV3, and filamentation in the haloarchaeon Haloferax volcanii.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Plasmid. SEQUENCE 255 AA; 27018 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U95375; AAB71809.1; -. HSSP; O70351; 1E6W.
                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charlebois R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=DS2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halobacterium volcanii (Haloferax volcanii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Farahani R., Imbeault J.-C., St Jean A., Chan C.C.-Y., Allard G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
                                                                                                               190
                                                                                                                                                                                             130 AVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYGVRVGAV 189
                                                                                                                                      190 LPGPVVTALLDDWPKAKMEEALAN··GSL··MQPIEVAESVLFMVTRSKNVTVRDLVILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
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                                                                                                                                                                                                                                                                                          13 LNGKVAAITGAASGIGLQCAKTLLDAGAKVVLIDREGDKLHKIVAEL---GENAYALQLD
                                                                                                                                                                                                                      70 VTVDDDIDALVEATLDEHGRIDILVNNAGLMPLAHIGEADRETLQTTIDVNLTGLITLTH
                                                                                                                                                                                                                                                  70 LFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAFRCVR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SDR) FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRCVRAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVNAVGAGFVDTPLMAGRDPEW-LAAVAASHPLGRLAQPDEIASVVAFLASSAASFVTGA 235
                                                                                                            EPGAVDTELLDHIPDEEVQKNVKDYVGTMDALAPEDIARTITFVVTQPERVDINEVLIRP
                                                                                                                                                                   AVVPTMMEQESGHIVNLSSVVGRFLQANSSHYNAAKAGVKMFSDSLRLDVAEAGIHVSSI
                                                                                                                                                                                                                                                                             LDGKVAIVTGASSGIGSATAKSLASRGASVVVAARREGELEELAATIEDDGGDALVVPTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVGAVLPGPVVTALL----DDWPKAKMEEALANGSLMQPIEVAESVLFMVTRSKNVTVRD 240
                                                                                                                                                                                                                                                                                                                                      72;
                                                                                                                                                                                                                                                                                                                                                 Similarity
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 (TrEMBLrel. 16, (TrEMBLrel. 16,
                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                23.4%; Score 295.5;
30.0%; Pred. No. 2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05,
19,
                                                                                                                                                                                                                                                                                                                                   57; Mismatches 104;
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Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                   No. 2.5e-15;
                                         248
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Best Local Similarity
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-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASI
(SDR) FAMILY.
EMBL; AJ012346; CAC20627.1; -.
HSSP; 070351; 1E6M.
                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0080: SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
Hypothetical protein; Oxidoreductase.
SEQUENCE 248 AA; 26849 MW; 992CB93B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hain T., Pashalidis P., Hudel M., Chakraborty "Nucleotide sequence of the internalin operon monocytogenes EGD.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.8 kDa protein.
Listeria monocytogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; B
Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=EGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                            187
                                                                                                                                                       129
                             242 VILPGS
                                                           182 VTIYPAAINTELLETITDKETEQGMT--SLYKQYGITPDRIASIVAYAIDQPEDVNVNEF
                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                  69 DIFNNQQVDNMLADIIELAGGLDIFHANAGAYIGGPVAEGDPDVWDRVLNLNINAAFRCV
                                                                                                                                                                                                                                                 3 IKNKVIIITGASSGIGKATALLLAEKGAKLVLAARRVEKLEKIVQTIKANSGEAIFA-KT
TVGPTS
                                                                                                                                          RAVLPHMIAQRSGDIIFTSSIAGVVPVIWEPIYTASKFAVQAFVHTTRRQVSQYG--VRV 186
                                                                                                                                                                                      DVTKREDNKRLVELAIERYGKVDAIFLNAGIMPNSPLSALKEDEWEQMIDINIKGVLNGI
                                                                                          GAVLPGPVVTALLDDWPKAKMEEALANGSL-----MQPIEVAESVLFMVTRSKNVTVRDL
                                                                                                                         AAVLPSFIAQKSGHIIATSSVAGLKAYPGGAVYGATKWAVRDLMEVLRMESAQEGTNIRT
                                                                                                                                                                                                                                                                                                                 79;
                               247
245
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                              23.1%; Score 292; DB 2; Length 24 32.1%; Pred. No. 4.4e-15; tive 47; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                              992CB93B9EC011D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T., Domann E.;
from Listeria
                                                                                                                                                                                                                                                                                                                                             Length 248;
                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                              Gaps
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l: /SIDS1/gcgdata/
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Listing first 45 summaries
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Drosophila melanog
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Propionibacterium
Bacillus subtilis
Staphylococcus
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S. epidermidis ope	AAG82195	22	499		255.5	45
Staphylococcus epi	ABP39502	23	514	2	259	4 4
lmonella t	AAU38195	22	501		262.5	42
taphylococ	AAU36742	22	498		264.5	41
Staphylococcus	AAU33825	22	496		264.5	40
Thermus flavus	AAW94309	20	496	9.4	264.5	39
Klebsiella oxytoca	AAY70727	21	501	9.4	265.5	38
Glycerol kinase	AAW06440	17	498	9.4	265.5	37
Propionibacterium	AAU60271	22	526	9.6	269	36
Drosophila melanog	ABB66928	22	538		272	35
Streptococcus	AAU38067	22	502		273.5	34
Streptococcus	AAU37838	22	502	•	276.5	33
E. coli cellular	AAU34832	22	502	9.8	276.5	32
Heat-resistant	AAW94843	20	497		276.5	31
Streptococcus	ABP26833	23	502		277.5	30
Corynebacterium g	AAB79335	22	509	9.9	279.5	29
C glutamicum prote	AAG92932	22	509		279.5	28
ococcus	ABP26834	23	508	0		27
Staphylococcus	AAU34300	22	509	0.2	288 1	26
Staphylococcus	AAU37244	22	517	0.	9	25
ť	ABP39566	23	497	0.	93.5	24
S. epidermidis	AAG82146	22	496	0.5		23
=	ABB48654	23	497	0.	98.5	22
	548	22	503	0	02.5	21
Enterococcus faeca	AAU35273	22	501	0.	ω	20
Putative P. abyss	AAB96826	22	494	0		19
Lactococcus lact	ABB54582	23	498	0.		18
-	AAU34790	22	484		306 1	17
Lactococcus lactis	ABB55539	23	519	1.0	9	16
Listeria monocytog	746	23	504	1.3	7	15
¢	ABP27721	23	518	1.4	2	14
Streptococcus	48	23	505	1.4	را ا	3
Ē	20	22	164	1.7	330 1	12
S. epidermidis	AAG82039	22	521	1.8	330.5 1	11

ALIGNMENTS

AAE09780;

29-NOV-2001 (first entry)

Escherichia coli strain C rtl operon encoding ribitol kinase

AAE09780 standard; Protein; 534 AA.

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RESULT 1
AAE09780
ID AAE0
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KW Posi
KW ribi
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Positively selecting transformed cells comprising selectable marker
                                                                                               N-PSDB, AAD16811.
                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000; 2000US-0188291.
15-AUG-2000; 2000US-0255595.
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                                                                                                                                                  WPI; 2001-565596/63.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used in positively selecting transgenic cells from a population of cells using the positive selection method, the presence of the gene of interest in the genetically transformed cells may be determined without the disadvantages associated with traditional negative selection systems. Positive selection of the transformed cells is achieved without directly damaging the neighbouring non-transformed cells. The transformed cells may be identified by simple visual means without the use of a separate assay to determine the presence of a marker gene. This technique also avoids the release of antibiotics or other dangerous genes into the environment. The present sequence is Escherichia coll strain C ribitol kinase encoded by ribitol operon (rtl operon). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a positive selection system that involves conferring to transferred cells the ability to metabolise analyte, ribital and/or mannitol. The positive selection method is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene a
               23-SEP-2002
                                             AAE24140;
                                                                          AAE24140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain C ribitol kinase encoded by ribitol operon (rtl operon). The operon also encodes ribitol dehydrogenase and ribitol transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                  GAVAGNIAPSVGEAMQQFTHVDKYYYPQERYQSLHHRRYEAYKQLQHTAKLLRD
                                                                                                                                                                                                                                                                          TAQPSDAVALAKGLHVVPEFLGNRAPFADPHARAVICGLGMERDLDNLLALYIAGLCGIG
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Query Match Best Local Matches

Similarity

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Conservative

96;

Pred. No. 4.3e 5; Mismatches Score 1172; DB 23; Pred. No. 4.3e-107;

Indels Length

18;

Gaps

67

Sequence

551 AA;

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cc treating and preventing cancer, an immune system disorder (e.g., carquired immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma, atherosclerosis, multiple sclerosis, psoriasis), disorders casthma, atherosclerosis, multiple sclerosis, psoriasis), disorders (e.g., fatty cast), and development (e.g., arteriosclerosis, cirrhosis, hepatitis), cardiovascular disorder (e.g., fatty cast), and a lipid disorder (e.g., fatty cast), and for assessing the effects of exogenous compounds. Anti-PKIN antibody is useful in a diagnostic test for a condition or a disease associated with the expression of PKIN in a susful for treating a disease or condition cantagonist of priore and composition comprising PKIN or an agonist or antagonist of PKIN is useful for treating a disease or condition cassociated with decreased or increased expression of functional PKIN. PKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN DNA is useful for creating a condition condition condition condition and condition condition of a sociated with decreased or increased expression of functional PKIN. The present sequence is human diseases, and in somatic or germline gene therapy. The present sequence is human diseases.
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27-OCT-2000;
03-NOV-2000;
09-NOV-2000;
16-NOV-2000;
22-NOV-2000;
01-DEC-2000;
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Lal PG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates human kinases (PKIN) and their corresponding nucleic acid sequences. PKIN and its DNA are useful for diagnosing,
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R, Lu Y, Yue H, Burford
Recipon SA, Lu DAM, Bor
Lu K, Khan FA, Ison CH;
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"Burford N, Bandman O, Tri

Barrowsky ML, Thornton
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g YT, Hafalia AJA, Nguyen DB;
mandman O, Tribouley CM;
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25-APR-2000;
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19-JUL-2000;
03-AUG-2000;
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19-OCT-2000;
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2000US-0553317.
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Note: The sequence
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as central nervous system injuries -
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 GAAVLGACASGDFASVQEAMAKMSKVGKVVFPRLQDKKYYDKKYQVFLKLVEHQKEYL 545
                                                                                                                                                   I-LEKTAQPSDAVALAKGLHVVPEFLGNRAPFADPHARAVICGLGMERDLDNLLALYIAG
                                                                                                                                                                               PGVWGPYFSAMVPGFWLNEGGQSVTGKLIDHMVQGHAAFPELQVKATARCQSIYAYLNSH
                                                                                                                                                                                                                                                                                                       VCKWTYSA-EKGWDDSFWKMIGLEDFVADNYSKIGNQVLPPGASLGNGLTPEAARDVGLL
                                                                                                                                                                                                                                                                                                                        TCKWTWLAHENRWDPDYFRTIGLAELADEDFIRIGHHIVSPGTPCGNGLTAQAAAEMGLL
                                                                                                                                                                                                                                                                                                                                                                                 HPVLNYVGGKISPEMETPKILWLKENMPEI-YERAGQFFDLADFLTWRATGDLARSVCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADVCAQSVAGIGFDATCSLVVLDKNGDPLPVSPEGDAKQNIIVWMDHRATEQAERINATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGVDVGTGSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACCVVTKKVVQG
                          GSAILGAVAGNIAPSVGEAMQQFTHVDKYYYPQERYQSLHHRRYEAY-KQLQHTAKLL 532
                                                           VQAIALGTRFIIEAMEAAGHSISTLFLCGGLSKNPLFVQMHADITGMPVVLSQEVESVLV
                                                                           LDLIKKAQP--VGFLTVDLHVWPDFHGNRSPLADLTLKGMVTGLKLSQDLDDLAILYLAT
                                                                                                                                                                                                            PGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLDFHPAVEEAREMAQRVNQPLPVWLADR
                                                                                                                                                                                                                                            PGIAVAASLIDAHAGGLGVIGADVRGHGLICEGQPVTSRLAVICGTSSCHMGISKDPIFV
                                                                                                                                                                                                                                                                      PGTPVAVGLIDAHAGGIGTVG--VEGGAL-----NNLAYVFGTSSCTMASTTSPSFV
                                                                                                                                                                                                                                                                                                                                                                   HSVLQYVGGVMSVEMQAPKLLWLKENLREICWDKAGHFFDLPDFLSWKATGVTARSLCSL
                                                                                                                                                                                                                                                                                                                                                                                                                             IDL--NQIRGLGFDATCSLVVLDKQFHPLPVNQEGDSHRNVIMWLDHRAVSQVNRINETK
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Zhou P,
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Goodrich R,
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Pred. No. 5.5e-107;
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Best Local
                                                                                                                                                                                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The inventueseful in developmental biology and in elucidating cell signalling cell: cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ
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11-JUL-2000;
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GTVVSTSLIDAHAGALGMEGCRSKESKGADDVQG----KMALIAGTSTCHMSITRKACEA
                                                         CKWTWLAHENRWDPDYFRTIGLAELADEDFIRIGHHIVSPGTPCGNGLTAQAAAEMGLLP
                                                                                       HPVLNYVGGKISPEMETPKILWLKENWPEIYERAGQFFDLADFLIWRATGDLARSVCTVT
                                                                                                                                   GGVDKSKVKGIGFDATCSLVVLGPQGSPLTVSKSGEAEQNIILWMDHRAEQETQEINAFK
                                                                                                                                             ADVCAQSVAGIGFDATCSLVVLDKNGDPLPVSPEGDAKQNIIVMMDHRATEQAERINATH
                                                                                                                                                                            IGVDVGSGSVRAGIFDLNGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNALTL
                         GTPVAVGLIDAHAGGIGTVG:
                                            CKWNYDAANGSWNKEFLKQADLEELTQNNFEKLGSDVQPPGRTVGKGLTAKAAGELGLSA
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2000US-0614150
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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                                                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                 Human;
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Sugiyama
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2000JP-0118776.
2000JP-0183767.
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1 T, Wakama
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    SQVGCLTQDVHVWPDLHGNRSPIADPTLRGVITGLDMTRGTESLA

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to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to zequence and an oligonucleotide comprises a 3'-end sequence, where the oligonucleotide which comprises a 1-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in

of

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary

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Best Local Sim
Matches 127;
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                                                                                                                                                                                                                                                                  21-APR-2000; 2000US-199047P
02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU39145 standard; Protein; 554
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                                                                                                                       L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                      20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                             (CORI-) CORIXA
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                                                                2001-616774/71
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                                                                                                                    Mitcham JL, Wang
, Jen S, Carter
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Example 1; SEQ ID No
                                                                                                                                                     treating acne vulgaris
                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                        340; 1069pp; English
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the treatment, prevention and diagnosis of medical conditions caused by
CP. acnes The disorders include SAPHO syndrome (synovitis, acne,
pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CP. acnes is also involved in infections of bone, joints and the central
CN nervous system, however it is particularly involved in the inflammatory
CN lesions associated with acres in a patient comprises contacting the
CN presence or absence of P. acnes in a patient comprises contacting a
CN sample with a binding agent that binds to the proteins of the invention
CN and determining the iamount of bound protein in the sample. The
CN polypeptides may be used as antigens in the production of antibodies
CN consequiate expression and activity of P. acnes polypeptides and
CN consequiate expression and activity of P. acnes polypeptides and
CN consequiate expression and activity of P. acnes polypeptides and
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CN the consequence da Sequences AAU39105-AAU68017 represent Propionibacterium acnes polypeptides. The proteins and their associated DNA sequences Sequence ftp.wipo.int/pub/published_pct_sequences. 554 AA; immunogenic are used in

Matches Query Match Best Local (h 19.7%; Score 553.5; DB 22; Similarity 28.7%; Pred. No. 1.1e-45; 54; Conservative 85; Mismatches 227; Length 71; Gaps 12;

311 199 139 363 303 254 243 183 126 88 67 28 7 VIGVDVGSGSVRAGIFDLNGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNALT LLGIDYGTESCRVAIFDLAGRPLTFAATPYKTTHPRPGWAEQDPEEWWKALQASCHRAIA QPSDAVAL - - - - -YYSAMVPGLWLVEGGQSAAGAAIDQLLDFHPAVEEAREMAQRVNQPLPVWLADRILEKTA THHPVLNYVGGKISP----EMETPKILWLKENMPEIYERAGQFFDLADFLTWRATGDLARS LADVCAQSVAGIGFDA-TCSLVVLDKNGDPLPVSPEGDAKQNIIVWMDHRATEQAERINA YSDAVMPGQYTVEGSQVSTGSVLK---LGLRPGIPVAQGLGDAWAGQIG-LGVL--APGSMALITGSSHVLTGQSDTEIHGEGFFGA MGLLPGTPVAVGLIDAHAGGIGTVGVEGGALNNLAYVFGTSSCTMASTTSPSFVPGVWGP INSAAIRMYYNRDKGGWPEDFYETIG----CDDVFDKIPGRVLDLGTPVGT-LGTIPAQL VCTVTCKWTWLAHENRWDPDYFRTIGLAELADEDFIRIGHHIVSPGTPCGNGLTAQAAAE SDSVARLYNGAGVSPATAEXYPFKAAWLRDHEPETYRRAAHLVDAPDWVTFKLTGEWTTN AAGISPAAIAGISYDATTLTMVAMDERGNEL --RPAMMWMDVRATEQAARAEN WEKDNEAADYT 406 362 310 302 253 198 138 87 66

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RESULT 7
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TEVGDAVVLGTCMVAAVGAGLFKDLPEAATQMVHEIDFIEPDQER---

HEEYQYY

TQCCEPVLLGSAILGAVAGNIAPSVGEAMQQFTHVDKYYYP-QERYQSLHHRRYEAY

NLLALYIAGLCGIGYGLRQILDAQTAQGVVSKNIVISGGAGQHPLVRQILADTCGIPVIT AAAEKIGLNPYDVLNEQSRNIRPGSDGLIINEYFQGNRTPYTDSKARGIIWGLSLMHTPA

HFYHAIQESVC---YGTAHNLRAMKAAGFEVDRMVACGGATKSRDWIQMHADVPGVPIVL

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                   This polypeptide comprises the L-ribulokinase of Bacillus subtilis, encoded by the araB gene of the ara operon (see AAV This enzyme is involved in the utilisation of L-rabhonse by B subtilis. The invention relates to the strong promoter (s AAV25567) of the ara operon, which is induced by L-arabinose repressed by glucose, and its use in regulating the expression heterologous genes in prokaryotic hosts.
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heterologous protein ε
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  GVHELLSEKANHQAPG
                                                                                                   GTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIGTVGV-EGGALNNLAYVFGTSSCT
                                           VLLGEEVHIVPGMCGVVDNGILPGYAGYEAGQSCVGDHFDWFVKTCVPPAYQEEAKEKNI
                                                              MASTTSPSFVPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLD--FHPAV-EEARE---
                                                                                       GEKAGS-LTEKMAKLTGLLPGTAVAVANVDAHV-SVPAVGITEPG---KMLMIMGTSTCH
                                                                                                                                   DWIVYQLCGSLKRSNCTAGYKAMWSEKAGYPSDDFFEKLNPSMKTITKD--KLSGSIHSV
                                                                                                                                                        DFLTWRATGDLARSVCTVTCKWTWLAHENRWDPDYFRTIGLA-ELADEDFIRIGHHIVSP
                                                                                                                                                                                 HHAAQKHADRLNQIAEEEGEAFLQRYGGKISSEWMIPKVMQIAEEAPHIYEAADRIIEAA
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                    MAQRVNQPLPVWLADRILEKTAQPSDAVALAKGLHVVPEFLGNRAPFADPHARAV
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27.1%;
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                                                                                                                                                                                                                                                                                                                                          Score 448.5;
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 ESGLLALDWWNGNRSTLVDADLTGM
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pustulosis, hypertosis and ostcomyelitis), uvcitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with ache vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by

polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

immunogenic are used in

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02-JUN-2000;
07-JUL-2000;
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pphthalmitis; bone; joint; central nervous system; ELISA;
lesion; acne vulgaris; enzyme linked immunosorbent assay;
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27-AUG-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                     07-FEB-2001
                                                                                                                  EP1074617-A2
                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                  FCDICRVPLSVGTIKQPGAHGSAVFAAVAADLYPDVKAASAAMGAKKAGVYQIDEQRAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                         LADTCGIPVITTQCCEPVLLGSAILGAVAGNIAPSVGEAM------QFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILGQTLTTTPED----QYRALLESTAFGARTIIESFRDSGVEINELVVAGGLTKNTFLMQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICGLGMERDLDNLLALYIAGLCGIGYGLRQILDAQTAQGVVSKNIVISGGAGQHPLVRQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRG-----IGVYDLLTEKCARQEVG---AHGLIALDWHNGNRSVLADANLSGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEAREMAQRVNQPLPVWLADRILEKTAQPSDAVALAKGLHVVPEFLGNRAPFADPHARAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SACYVVPGPQLKEVPGMFGVVDGGIVDGSWGFEAGQTAVGDIFAWFIDNCVPGSYFDEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSCTMASTTSPSFVPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLD-----FHPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LETLETIVRGAVKDAGVDPDHIVGIGLDVTSATVVAATKDGTPLCQLPEFRNEPHAWVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154;
                                                                                                                                                                                                   protein
                                                                                                                                                                       primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
 99JP-0248036.
99JP-0300253.
2000JP-0118776.
                                                         2000EP-0116126
                                                                                                                                                                                                                               (first entry
                                                                                                                                                                                                   sequence SEQ ID NO:12575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                        detection;
                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.5%;
                                                                                                                                                                       diagnosis; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
                                                                                                                                                                                                                                                                                       252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 435.5; DB 2
Pred. No. 6.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 263;
                                                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                                                                                                                        533
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                                                                                                                                                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77;
                                                                                                                                                                     therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89
                                                                                                                                                                                                                                                                                                                                                                                                                  541
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RESULT 10
ABP39224
ID ABP39
XX
AC ABP39

ABP39224 standard;

Protein;

518

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ABP39224;

B Qy В ν В δõ

LSQEVESVLVGAAVLGACASGDFASVQEAMAKMSKVGKVVFPRLQDKKYYDKKYQVFLKL TTQCCEPVLLGSAILGAVAGNIAPSVGEAMQQFTHVDKYYYPQERYQSLHHRRYEAY-KQ 524 DDLAILYLATVQAIALGTRFIIEAMEAAGHSISTLFLCGGLSKNPLFVQMHADITGMPVV

238

178 465 118 405 60

119 406

> DNLLALYIAGLCGIGYGLRQILDAQTAQGVVSKNIVISGGAGQHPLVRQILADTCGIPVI QSIYAYLNSHLDLIKKAQP--VGFLTVDLHVWPDFHGNRSPLADLTLKGMVTGLKLSQDL QPLPVWLADRI-LEKTAQPSDAVALAKGLHVVPEFLGNRAPFADPHARAVICGLGMERDL

DЪ δÃ

239 525 179

VEHQKEYL LQHTAKLL 532

246

δõ

287 MASTTSPSFYPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLDFHPAVEEAREMAQRVN 346

MGISKDPIFVPGVWGPYFSAMVPGFWLNEGGQSVTGKLIDHMVQGHAAFPELQVKATARC

Matches

98;

Conservative

45;

Mismatches

101;

Indels

4.

Gaps

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В

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347

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of an oligonucleotide comprising a sequence complementary to the CC complementary straind of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprises a 3'-end sequence complementary to a CC polynucleotide which comprises a 3'-end sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence, '-end sequence', '-end sequence is selected from those defined in CC the 5'-end sequence', '-end sequence is selected from those defined in CC the specification! The primer sets can be used in antisense therapy and CC in gene therapy. 'The primers are useful for synthesising polynucleotides, CC particularly full; length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CAAH3633 to AAH18/742 represent human cDNAs sequences; AAB92446 to AAH3633 to AAH18/742 represent human cand sequences; AAB9246 to AAH3632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of the specific complementary that the specific continuous combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific combination of the specific co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly full-length cDNAs defined in the specification, and for the and/or diagnosis of the abnormality of the proteins encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID 12575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAY-2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899
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                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     full-length cDNAs -
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   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugiyama T,
                                                                                                                     252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for synthesizing cDNAs defined in
                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishikawa T,
   15.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wakamatsu
Score 434; DB 22;
Pred. No. 2.4e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi K,
A, Nagai K,
                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               particularly the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Otsuki
                               Length
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                                          252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.B. The sequence data for this specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-2002
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   360
                                                                                                                                                        191
                                                                                                                                                                                                                    132
                                                                                                                                                                                       198
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                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                     NGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNALTLADVCAQSVAGIGFDATC 84
KTAQPSDAVALAKGLHVVPEFL-GNRAPFADPHARAVICGLGMERDLDNLLALYIAGLCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-381255/41.
DB; ABN91769.
                            AYEAGQPAVGDLFEYSKNQAPKHIVDQANEHHMPVLNYLEELASHI----
                                                         LVEGGQSAAG------AAIDQLLDFH-PAVEEAREMAQRVNQPLPVWLADRILE 359
                                                                                          PFIIDAHSGVLGVGAIEAG---EFTAVIGTSTCHLMLDSRQVPISSITGSVKNAIIPGLY
                                                                                                                       VGLIDAHAGGIGTVGVEGGALNNLAYVFGTSSCTMASTTSPSFVPGVWGPYYSAMVPGLW 312
                                                                                                                                                    GFNYDFFHSV-----DPDLPKIVKEKCEAPIISIGESAGR-LCKDYQQIWGLSQDVQVS
                                                                                                                                                                                  RWDPDYFRTIGLAELADEDFIRIGHH-----IVSPGTPCGNGLTAQAAAEMGLLPGTPVA 252
                                                                                                                                                                                                                 VNSEWMIPKILEVKHEAPEILRRARYIMEAGDYITSILTNSNIRSNCGIGFKGFW-DNEA 190
                                                                                                                                                                                                                                           ISPEMETPKILWLKENMPEIYERAGQFFDLADFLTWRATGDLARSVCTVTCKWTWLAHEN 197
                                                                                                                                                                                                                                                                            STIIFLDEQFEPL--HRHEDLKTNPHAYVKLWKHHGAQDEANYMIQMSKNKNWLDYYGSS 131
                                                                                                                                                                                                                                                                                                           SLVV-LDKNGDPLPVSPEGDAKQN----IIVWMDHRATEQAERI--NATHHPVLNYVGGK 137
                                                                                                                                                                                                                                                                                                                                          NGTYMNSLYDK----PLPGNYFLQNADDYLQILEQGVQFVLEDSKVNKNDVVGIGVDFTS 73
                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity
137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    518
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                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epidermidis;
gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epidermidis ORF amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-055779P.
97US-064964P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epidermidis
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                                                                                                                                                                                                                                                                                                                                                                                                                     12.18; 25.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        85;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 340; DB 23;
Pred. No. 1.6e-24;
15; Mismatches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patent did not form part of the printed in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                              ----RIEE 350
                                                                                                                                                                                                                                                                                                                                                                                                       82;
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418
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RESULT 11
AAG82039
ID AAG82
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AC AAG82
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AC AAG82
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DT 03-SI
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                     CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. CC (II) and (II) can have antibacterial activity and therefore can be used CC in vaccination. The nucleic acids (I) may be used to produce the CC s. epidermidis polypeptides (II) via the production of vectors CC containing them which are used to produce hosts cells which express the CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be CC used to vaccinate subjects and to raise antibodies against the bacteria. CC The polypeptides may also be used to assay for other inhibitors of their CC activity and therefore identify compounds that may be used for the CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to CC AAH55090 represent specifically claimed S. epidermidis genomic DNA CC Dolynucleotide sequences from the present invention. AAH55091 to CC CAAH55098 represent oligonucleotide sequences and primers which are used CC in the exemplification of the present invention. CC N.B. The present invention specifically claims all the polynucleotide sequences are given in the sequence for SEQ ID NO:4454 so even CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4454 so even
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kimmerly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis SR1 vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 337; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLAX ) GLAXO
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DB; AAH52889.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAFGTKLIMKQFEDNHIPVHTVYASGGIPQKSKLLVEIYANVLNKRVVVIDSSNASALGA
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Query Match
Best Local Similarity
Matches 135; Conser

Conservative

6;

Score 330.5; DB 22 Pred. No. 1.4e-23; 5; Mismatches 252;

DB 22;

Length 521;

65;

Gaps

17;

11.8%; 25.1%;

Sequence

521

δ

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AAM42079
ID AAM42
XX AAM42
AC AAM42
XX 22-OC
XX 22-OC
XX Perip
KW Human
KW Perip
KW Alzhe
KW Leuka
XX Homo
C W Chemo
C W 12-Ju
PD 26-JU
XX 21-Ju
PR 25-Ju
PR 25-Ju
PR 11-Ju
PR 13-Ju
PR 13-Ju
PR 13-Ju
PR 14-SE
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                              21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                 WO200153312-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM42079
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 (HYSE-)
                                                                                                                                                                                 26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                 26-JUL-2001
                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                  leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGIGFDATCSLVV-LDKNGDPLPVSPEGDAKQN----IIVWMDHRATEQAERI--NATHH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSAMVPGLWLVEGGQSAAGAAIDQLLDFHP---AVEEAREMAQRVNQPLPVWLADRILEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLSQYVQVSPFIIDAHSGVLGVGAIEAG---EFTAVIGTSTCHLMLDSRQVPISSITGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLLPGTPVAVGLIDAHAGGIGTVGVEGGALNNLAYVFGTSSCTMASTTSPSFVPGVWGPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGSLLSHATEKITTTRRSGSRVE------QSSQEIWQAVCSCIRNALTLADVCAQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGANVGNAYSTLKEAALSMKQ------PIAYIQEPEIQKVQAYKPLYHKYCELHD 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGAVAGNIAPSVGEA----MQQFTHVDKYYYPQERYQSLHHRRYEAYKQLQHTAKLLRD 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGTKLIMKQFEDNHIPVHTVYASGGIPQKSKLLVEIYANVLNKRVVVIDSSNASALGAAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGFW-DNEAGFNYDFFHSV-----DPDLPKIVKEKCEAPIISIGESAGR-LCKDYQQIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KWTWLAHENRWDPDYFRTIGLAELADEDFIRIGHH----IVSPGTPCGNGLTAQAAAEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGIGVDFTSSTIIFLDEQFEPL--HRHEDLKTNPHAYVKLWKHHGAQDEANYMIQMSKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGHIISRYEEDYANGTYMNSLYDKPLPENYFLQNADDYLQILEQGVQFVLEDSKVNKNDV
                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide SEQ ID NO 7010
 HYSEQ
                              2000US-0488725.

2000US-0552317.

2000US-0598042.

2000US-0620312.

2000US-0652450.

2000US-0652191.

2000US-0693036.

2000US-0693036.
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human nucleic acids (AA157798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity. Prager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang
Wang
                                                                                                                                       Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao
                                                                                                                                     group A streptococcus; Streptococcus;
antiinflammatory; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.N.S disorders.
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27-OCT-2000;
24-NOV-2000;
                                                                                                                                                                                          Streptococcus polypeptide SEQ
                                                                                                                                                                                                                  02-JUL-2002
                                                                                                                                                                                                                                                                      ABP30486 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel
                                   29-OCT-2001; 2001WO-GB04789
                                                               02-MAY-2002
                                                                                                               Streptococcus agalactiae
                                                                                                                                                                                                                                              ABP30486;
                                                                                       WO200234771-A2
                                                                                                                                                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                                                                                                                                                      98
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                                                                                                                                                                                                                                                                                                                                                                                                  ADVCAQSVAGIGFDATCSLVVLDKNGDPLPVSPEGDAKQNIIVWMDHRATEQAERINATH 127
                                                                                                                                                                                                                                                                                                                                    HSVLQYVGG
                                                                                                                                                                                                                                                                                                                                                                                   VGVDVGTGSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACCVVTKKVVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acids and polypeptides, useful as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
2000GB-0026333.
2000GB-0028727.
                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                    164
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goodrich R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 330; DB 22;
Pred. No. 2.6e-24;
                                                                                                                                                                                           ID NO 10148.
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Ku C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
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Zhang
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07-MAR-2001;

2001GB-0005640

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus/GAS) comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is used to detect make whether a compound binds to used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used in gene therapy. Antibodies to (I) are used for affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus protein for the treatment or prevention or disease caused by Streptococcus bacteria, such as menir for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tettelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Telford J, Masignani V,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to a protein (ABP25413-ABP30895) from group
                                                                                                                                                                                                                                                 VSPGTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGTGTVGVEGGALNNLAYVFGTSS
                                                                                                                                                                                                                                                                                                                 RSVCTVTCKWTWLAHENRW------DP---DYF--RTI--GLAELADE-DFIRIGHHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLTTKSTKSQMIRAVYE----GIAFAHKQHITDLIKSRGSVPKIIRFSGGATNSPAWMQM
                                 GLGMERDLDNLL-ALYIAGLCGIGYGLRQ-ILDAQTAQGVVSKNIVISGGAGQHPLVRQI
                                                                                                       AREMAQRVNQPLPVWLADRILEKTAQPSDAVALAKGLHVVPEFLGNRAPFADPHARAVIC
                                                                                                                                            GTWNINTYPSLKPAKQDSGLMTSYFP---DRRYLLEASSPTSAGNLNFMLKMLMHQEIDN
                                                                                                                                                                           CTMASTTSPSFVP-----GVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLD--FHPAVEE
                                                                                                                                                                                                                --PG-----GISSQAAKETGLVEGTPVVGGLFDIDACALGSGVLESD------TFSVIS
                                                                                                                                                                                                                                                                                    QEYGD-----ASGNHWINFQTGTYDPAILDFFGIREIENSLPELIDSADLV-----
                                                                                                                                                                                                                                                                                                                                                        YFESKLDNIWELTRQHIFPS-QSPVILRWLKDYQPETYKSIGAVLSAKDFIRYKLTGKVQ
                                                                                                                                                                                                                                                                                                                                                                                           RINATHHPVLNYVGGKISPEMETPKIL-WLKENMPEIYERAGQFFDLADFLTWRATGDLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                            ISKLSPEQISAV----ACIGHGKGLYLLDNKLEPL-----EQGILSTDNRAKDLAQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LADVCAQSVAGIGFDATC-----SLVVLDKNGDPLPVSPEGDAKQNIIVWMDHRATEQAE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGVDVGSGSVRAGIFDLNGSLLSHAT-EKITTTRRSGSRVEQSSQEIWQAVCSCIRNALT 66
                                                                      AKSSGGSIYDNLEEFL--
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DB; ABN71117.
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INST GE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 4144-4145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 1.3e-22;
                                                                      THTDATHHGLIFFPFLYGSN---TSQDASACFF
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ences (S1), given in
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Best Local Si Matches 141; Query Match

Similarity

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Conservative

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Score 320.5; DB 23 Pred. No. 1.4e-22; 4; Mismatches 231;

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                                    The invention relates to a protein (ABP25413-ABP30895) from group B Streptcocccus/GBS (Streptcocccus agalactiae) or group A streptcocccus/GAS (Streptcocccus/GAS (Streptcocccus/GAS), given in C (Streptcocccus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention, of infection or disease caused by Streptcocccus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptcocccus in a Diological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                    New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
Sequence
                                                                                                                                                                                                                                                                                                       Claim 1; Page 3623; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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24-NOV-2000;
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; 2001GB-0005640.
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Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Deho Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cos Daniels J, Goobel W, Kreft J, Kuhn M, Ng E, Væxquez-Boland Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Ame Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Duran Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLTTKSTKSQMTRAVYE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIGMERDLDNLL-ALYIAGLCGIGYGLRQ-ILDAQTAQGVVSKNIVISGGAGQHPLVRQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for blosynthesis and biodegradation, especially biosynthesis of Vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, related polypeptides {}^{\dagger}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did no specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccines compositions for the treatment or prevention monocytogenes and related organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTSKPYIMGVDIGTSSTKAVLFNQRGEVIFRQATHYELITDETG-KAEESPTEIFDAVLT
SLHHRRYEAYKQLQHTAK 530
                                  EIRVPHTIEGSSLGAAIIGMRSLGILKDLN--LKHTLPIKAVYHPSENVLKYAELRLIFK
                                                                                                           TINHTKAHFIRAILEGVAFNLAEVYEAVSAPDDI---IYVTGGISAHDAWCKLLADILNR
                                                                                                                                            DLDNLLALYI-AGLCGIGYGLRQILDAQTAQGVVSKNIVISGGAGQHPLVRQILADTCGI
                                                                                                                                                                                                                  RVNQPLPVWLADRILEKTAQPSDAVALAKGLHVVPEFLGNRAPFADPHARAVICGLGMER
                                                                                                                                                                                                                                                                                             ---TSPSFVPGVWGPYY---SAMVPGLWLVEGGQSAAGAAID-QLLDFHPAVEEAREMAQ
                                                                                                                                                                                                                                                                                                                                   VKKEYAELMGIPENLPFIIGGSD----GALANIGIQATGQNDVTITVGTSGAVRKLTDQFQ
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                                                                     PVITTQCCEPVLLGSAILGAVAGNIAPSVGEAMQQFTHVDKYYYPQER-
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Scoring table:

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US-09-134-001C-4411
US-09-172-952-26
US-09-172-952-15
US-09-134-001C-4347
US-09-134-001C-4347
US-09-134-001C-43170
US-09-134-001C-43170
US-09-172-952-27
US-09-172-952-27
US-08-969-683A-18
US-09-297-928-15
US-09-370-700-5
US-09-370-700-5
US-08-967-970-3
US-08-967-970-3
US-08-967-229-2
US-08-967-229-2
US-08-967-229-2
US-08-967-239-40
US-09-108-020-6
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US-08-926-842B-18
                             US-09-320-878-2
US-09-105-537-33
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                                                               Sequence 13, Appl Sequence 19, Appl Sequence 26, Appl Sequence 27, Appl Sequence 11, Appl Sequence 27, Appl Sequence 15, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 28, Appl Sequence 38, Appl Sequence 48,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                        Sequence
Sequence
                     , 33,
Appli
3, Appli
Appli
                                                                                                                                                                                                                                                                                                    ZIP: 07601

ZIP: 07601

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURENTY APPLICATION NUMBER: US/08/926,842B

FILING DATE: 10-SEP-1997

CLASSIFICATION: 10-SEP-1997

CLASSIFICATION: 1435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-089

TELEPHONE: 201 487-5800

TELEPAX: 201 343-1684

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

FENCTH: 560 amino acids
                                                                                                                    ; OTHER INFORMATION: /product= "arab" US-08-926-842B-13
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US-08-926-842B-13
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                        Query Match
Best Local Similarity
Matches 153; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Sa-No. 6030807ueira, Isabel
APPLICANT: de Lencastre, Herminia
TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                    MOLECULE TYPE: p
ORIGINAL SOURCE:
ORGANISM: Baci
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                          LENGTH: 50
TYPE: amin
TOPOLOGY:
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COUNTRY: USA |
ZIP: 07601
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CITY: Hackensack
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US-09-413-814-48
US-09-436-987A-3
US-09-370-700-3
US-08-746-283-3
US-09-408-647A-2
US-09-408-647A-2
US-08-694-865-17
US-08-535-837-3
US-09-124-491-17
US-08-583-837-3
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                             Mismatches
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Sequence 2, Appli
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Sequence 2, Appli
Sequence 3, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
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RESULT 2
US-08-926-842B-18
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                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/08926842B
Patent NO. 6030807
GENERAL INFORMATION:
APPLICANT: Sa-No. 6030807ueira, Isabel
APPLICANT: de Lencastre, Herminia
APPLICANT: HIGHLY REGULABLE PI
             NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                             SOFTWARE: Patentin Reli
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
                                                                   APPLICATION NUMBER: US/0
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           STREET: 411 Hack
CITY: Hackensack
  TELEPHONE:
                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILADTCGIPVITTQCCEPVLLGSAILGAVAG-----NIAPSVGEAMQQFTHVDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HHAAQKHADRLNQIAEEEGEAFLQRYGGKISSEWMIPKVMQIAEEAPHIYEAADRIIEAA
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                                                                                                                                                                                                                                                New Jersey
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                                                                                                                                                                                                                                    USA
                                                                                                                                              PatentIn Release #1.0,
  487-580C
                                                                                                                                                                                                                                                                                                                                     EXPRESSION
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                                                                                                                                                                                                                                                                                            Jackson
                             600-1-089
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US-08-926-842B-19
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Matches
                                                                                                                                            Patent No.
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                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201 343-1684 |
TELEX: 133521
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                          437
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STREET:
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                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
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                                                                                                                                              6030807
             411 Hackensack
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                            Klauber & Jackson
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Sequence 19, Application US/08926842B
APPLICANT: Sa-No. 6030807ueira, APPLICANT: de Lencastre, Hermin TITLE OF INVENTION: HIGHLY REGUITITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 RHHPRDYIESMEAALKTVLAELSVEQRAAVVGIGVDSTGSTPAPIDADGNVLALRPEFAE 110
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Local Similarity 27.6%;
Les 163; Conservative 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLRQILDAQTAQGVVSKNIVISGG-AGQHPLVRQILADTCGIP----VITTQCCEPVLLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAWAKNPSLDHLPVVLDWFNGRRSPNANQRLKGVITDLNLATDAPLLFGGLIA---ATAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VALAKG-----LHVVPE-FLGNRAPFADPHARAVICGLGMERDLDNLLALYIAGLCGIGY 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAFGDIYAWFGRVLSWPLEQLAAQHP----ELKAQINAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFFDELDPILNRHLPSPLFTDTWTADIPVGT-LCPEWAQRLGLPESVVISGGAFDCHMGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGVDVGSGSVRAGIFDLNGSLLSHATEKITTTRRSGSRVEQSSQEIWQ--AVCSCIRNAL 65
                                                                                                                                                                                                                                                                                                                                      AIFAAVAAKVHADIPSAQQKMASAVEKTLQPRSEQAQRFEQL-YRRYQQW
                                                                                                                                                                                                                                                                                                                                                                                             AILGAVAGNIAPSVGEAMQQF-THVDKYYYPQ----ERYQSLHHRRYEAY 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GARAIMECFTDQGIAVNNVMALGGIARKNQVIMQACCDVLNRPLQIVASDQCC---ALGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAAGA-----AIDQLLDFHPAVEEAREMAQRVNQPLPVWLADRILEKTAQPSDA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQSAASWIELCDWVPALLSGTTRPQDIRRGRCSAGHKSLW--HES-WG-----GLPPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGTVGVEGGALNNLAYVFGTSSCTMASTTSPSF----VPGVWGPYYSAMVPGLWLVEGGQ
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HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS
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Pred. No. 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 569 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-089
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                444 CFTDQGIAVNNVMALGGIARKNQVIMQVCCDVLNRPLQIVASDQCC---ALGAAIFAAVA
                                                                                                                                           373 GLHVVPE----FLGNRAPFADPHARAVICGLGMERDLDNLLALYIAGLCGIGYGLRQILD 428
                                                                                                                                                                                341 IYAWFSRVLSWPLEQLAAQHPELKPQINASQK--QLLPAL-----TDAWAKNP
                                                                                                                                                                                                                                                                                     268 VEGGALNNLAYVFGTSSCTMASTTSPSF----VPGVWGPYYSAMVPGLWLVEGGQSAAGA 323
                                                                                                                                                                                                                                                                                                                               226 LDPCINRHLRYPLFSETFTADLPVGT-LCAEWAQRLDLPESVVISGGAFDCHMGAVGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 FYLWKDHTAVEEADEITRLCHKPGKVDYSRYIGGIYSSEWFWAKILHVTRQDSAVAQAAV
485 GNIAPSVGEAMQQF-THVDKYYYPQ----ERYQSLHHRRYEAY 522
                                                                                                                                                                                                                                                                                                                                                                                                                                         163 QFFDLADFLTWRATG-----DLARSVCTVTCKWTWLAHENRWDPDYFRTIGL--AELADE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 IIVWMDHRATEQAERINATHH-----PVLNYVGGKISPEMETPKILWLKENMPEIYERAG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/926,842B FILING DATE: 10-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 MESMEAALKAVLAQLSAAQ--RANVVGIGVDSTGSTPAPIDADGNVLALRPEFAENPNAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 QEIWQAVCSCIRNALTLADVCAQSVAGIGFDATCSL-VVLDKNGDPLPVSPEGDAKQN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocal Similarity
                                                                    AQTAQGVVSKNIVISGG-AGQHPLVRQILADTCGIP---VITTQCCEPVLLGSAILGAVA 484
                                                                                                       SLDHLPVVLDWFNGRRTPNANQRLKGVITDLNLATDAP---ALFGGLVASTAFGARAIQE
                                                                                                                                                                                                                                                        --GAQPNTLVKVIGTSTCDILIADKQSVGDRAVKGICGQVDGSVVPNFIGLEAGQSAFGD 340
                                                                                                                                                                                                                                                                                                                                                                  DFIRIGHHIVSP-----GTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIGTVG
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US-09-134-001C-4069
US-09-134-001C-4069
Sequence 4069, Application US/09134001C
Patent No. 6380370
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LENGTH: 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND ANNO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 518
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
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455 AMLGANVGNAYSTLKEAALSMKQ--
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                                                                                        395 TAFGTKLIMKQFEDNHIPVHTVYASGGIPQKSKLLVEIYANVLNKRVVVIDSSNASALGA
                                                                                                                                                                                                                                                                                                                                                                            244 PFIIDAHSGVLGVGAIEAG---EFTAVIGTSTCHLMLDSRQVPISSITGSVKNAIIPGLY 300
                                                                                                                                                                                                                                                                                                                                                                                                                        253 VGLIDAHAGGIGTVGVEGGALNNLAYVFGTSSCTMASTTSPSFVPGVWGPYYSAMVPGLW 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity nes 137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 STIIFLDEQFEPL--HRHEDLKTNPHAYVKLWKHHGAQDEANYMIQMSKNKNWLDYYGSS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 NGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNALTLADVCAQSVAGIGFDATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFNYDFFHSV-----DPDLPKIVKEKCEAPIISIGESAGR-LCKDYQQIWGLSQDVQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RWDPDYFRTIGLAELADEDFIRIGHH-----IVSPGTPCGNGLTAQAAAEMGLLPGTPVA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISPEMETPKILWIKENMPEIYERAGQFFDLADFLTWRATGDLARSVCTVTCKWTWLAHEN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLVV-LDKNGDPLPVSPEGDAKQN----IIVWMDHRATEQAERI--NATHHPVLNYVGGK 137
                                       AILGAVAGNIAPSVGEA----MQQFTHVDKYYYPQERYQSLHHRRYEAYKQLQHTAKLLRD 534
                                                                                                                                    IGYGLRQILDAQTAQGVVSKNIVISGGAGQ-HPLVRQILADTCGIPVITTQCCEPVLLGS 477
                                                                                                                                                                                                                                  KTAQPSDAVALAKGLHVVPEFL-GNRAPFADPHARAVICGLGMERDLDNLLALYIAGLCG 418
                                                                                                                                                                                                                                                                              AYEAGQPAVGDLFEYSKNQAPKHIVDQANEHHMPVLNYLEELASHI------RIEE
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                                                                                                                                                                                      VVLDWLNGNRSILSNSHLTGSIFGLTLQTPYEMIHRAYIE---A 394
-PIAYIQEPEIQKVQAYKPLYHKYCELHD 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 5 US-09-134-001C-4411

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RESULT 6
US-09-172-952-26
; Sequence 26, Application
; Patent No. 6368793
; GENERAL INFORMATION:
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APPLICANT: LYNN DOUGETTE-Stamm et al
APPLICANT: LYNN DOUGETTE-STAMM et al
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4411
FERCELL 407
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Best Local Similarity
Matches 128; Conserv
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  APPLICANT: Hoch, James APPLICANT: Dartois, V. TITLE OF INVENTION: ME
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 RINATHHPVLNYVGGKISPEME---TPKILWLKENMPEIYERAGQFFDLADFLTWRATGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VKEVVLGIDLGTSAIKIIAVDQLGNVIESVSETLKLYQEHPGYSEQDPNEWFEATKKGIK
CANT: Dartois, Veronique
OF INVENTION: METABOLIC SELECTION METHODS
                                                                                                                                                                                                                      QSLHHRRYEAYKQLQHTAKLL 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MASTTSPSFVPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLDFHPAVEEAREMAQRVN
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                                                                                                                                                                                                 YSVYEAIYKQTKQL--TADLL 493
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                                                                                               US/09172952
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CURRENT APPLICATION NUMBER: US/09/172,95
CURRENT ETLING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.
SEQ ID NO 26
LENGTH: 498
TYPE: PRT
ORGANISM: LYXK-EC
US-09-172-952-26
                                GENERAL INFORMATION:
APPLICANT: Hoch, James
APPLICANT: Dartois, Veronique
TITLE OF INVENTION: METABOLIC SELECTION METHODS
FILE REFERENCE: 234/191
CURRENT APPLICATION NUMBER: US/09/172,952
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 501
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US-09-172-952-15
; Sequence 15, Application
; Patent No. 6368793
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Best Local Similarity
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ORGANISM: LyxK-Ko
                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --QAERINATHHPVLN---YVGGKISPEMETPKILWLKENMPEIYERAGQFFDLADFLTW | : | : | : | : | : | : | : | : | : |
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                                                                                                                                                                                                                                                                                                                                                                          KKYQRYQHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGLGMERDLDNLLALYIAGLCGIGYGLRQILDAQTAQGVVSKNIVISGGAGQHPLVRQIL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISFDEINQAVASLPKAGGDLFFLPFLYGSNA----GLEMTSGFYGMQA----IHTRAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCTMAST---TSPSFVPGVWGPYYSAMVPGLWLV-EGGQSAAGAAIDQLLDFHPAVEEAR 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATGDLARSVCTVTCKWTWLAHEN-----RWDPDYFRTIGLAELADEDFIRIGH---H 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RWQEDGIPEKLYPLTRQTLWTGHPVS-----LLRWLKEHEPERYAQIGCVMMTHDYLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADVSGLRIELPQVEETGCFGAALAARVGTGVYHNFSEAQRDLRHPVRTLLPDMTAHQLYQ
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; Pred. No. 4.7e-21;
77; Mismatches 243;
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516 413 396 317

368

283

210

266

173

165

62

22;

us-09-172-952-15

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RESULT 8

US-09-134-001C-4347

Sequence 4347, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: UCCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION UMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
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                                       Query Match
Best Local Similarity
                                                                                                                                                      SEQ ID NO 4347
LENGTH: 514
                     Matches
                                                                                                 ORGANISM: Staphylococcus epidermidis -09-134-001C-4347
                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 QALRVTGGPAHSDVWMQMLADVSGLRIELPKVEETGCFGAALAARVGTGVYRSFSEARRA 457
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nes 129; Conserv
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                     Conservative
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22.3%;
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                     82;
                   Score 259; DB 4;
Pred. No. 8.5e-18;
2; Mismatches 232;
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                                                       Length 514;
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US-09-134-001C-4170
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APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

TITLE OF INVENTION: EBPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4170 |
LENGTH: 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4170, Application US/09134001C Patent No. 6380370
                                                                                                                                    Matches
                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
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                     65
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LTLADVCAQSVAGTGF-DATCSLVVLDKN-GDPLPVSPEGDAKQNIIVMMDHRATEQAER 122
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                                                                                               KTVIGVDVGSGSVRAGIFDLNGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNA
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                                                         KYILSIDQGTTSSRAILFNKEGEIKGVSQREFKQHFPHPGWVEHDANEIWTSVLSVMAEL
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                                                                                                                                  al Similarity
117; Conserva
                                                                                                                                    Conservative
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                                                                                                                                                    9.18;
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                                                                                                                                    87;
                                                                                                                                  Score 255.5; DB 4;
Pred. No. 1.9e-17;
7; Mismatches 245;
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US-09-172-952-27
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US-09-172-952-27
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                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 27 LENGTH: 485
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 Application US/09172952
Patent No. 6368793
GENERAL INFORMATION:
APPLICANT: Hoch, James
APPLICANT: Dartols, Veronique
TITLE OF INVENTION: METABOLIC SELECTILE REFERENCE: 234/191
                                                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/172,952
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                           NILQKFYPITLQTLWMGHPVS-----ILRWIKENEPSRYEQIHTILMSHDYLRFCLTEK
                                                                                                                                                                         LGIDCGGTFIKAAIFDQNGTLQSIARRNIPIISEKPGYAERDMDELWNLCAQVIQKTIRQ 64
                             LARSVCTVTCKWTWLAHENRWDPDYFRTIGLAELADEDFIRIGHHIVSP---GTPCGNGL 235
                                                                                    RINATHHPV---LNYVGGKISPEMETPKILWLKENMPEIYERAGQFFDLADFLTWRATGD 178
                                                                                                                SSILPQQIKAIGISAQGKGAFFLDKDNKPL----GRA----ILSSDQRAYEIVQCWQKE 115
                                                                                                                                           ADVCAQSVAGIGFDAT-CSLVVLDKNGDPLPVSPEGDAKQNIIVWMDHRATE-----QAE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMDADQRHKLYSGWKK 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEVPIAGIAGDQQAALFGQACFDRGDVKNTYGTGGFMLMNTGE-EAVKSESGLLTTIAY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMAQRVNQPLPVWLAD--RILEKTAQP---SDAVALAKGLHVVPEFLGNRAPFADPHARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGTSSCTMASTTSPSFVPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLDFHPAVEEAR
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                                                                                                                                                                                                                                      129;
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----WLRDGLRMINSAPQTENYASRVESTEGVYMVPAFVGLGTPYWDSEARG
                                                                                                                                                                                                                                8.7%; Score 243.5; DB 4; 23.2%; Pred. No. 3e-16; tive 77; Mismatches 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GLDGKVNYAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                     SELECTION METHODS
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    VGFWDDKEDIRERWKLQTEFKP-

                                                                                                                                                                                                                                                            Length
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  LPPIIKSNKIAGYV
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US-08-968-563-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030
FILING DATE: NOVEMBER 13,
ATTORNEY/ACENT INFORMATION:
NAME: FLOYD, LINDA AXAMÉTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                       CITY: ROCHESTER STATE: NEW YORK COUNTRY: U.S.A.
                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                    CITY: WILMINGTON STATE: DELAWARE
                                                                                       FILING DATE:
                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                       COUNTRY:
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1007 MARKET STREET
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RAMESCH V. NAIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MARIA DIAZ-TORRES DONALD E. TRIMBUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHARON L. HAYNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RICHARD D. LA REAU
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    LINDA AXAMETHY
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
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                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD
SOFTWARE: MICROSOFT WORD VERSION
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: GENENCOR INTERNATIONAL, STREET: 4 CAMBRIDGE PLACE STREET: 1870 SOUTH WINTON ROAD
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US/08/968,563
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                                                                      7.0A
                                                                                                      FOR WINDOWS
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RESULT 12
US-08-969-683A-18
Sequence 18, Application US/08969683A
Patent No. 6136576
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                                                                                    GENERAL INFORMATION:
APPLICANT: GENENCOR
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 709 amino acids
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ORIGINAL SOURCE:
ORGANISM: GUT
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     477 SAILGAVAGNIA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 VECHPQKLLVNVVQCLASSLLSLQTINSERVANGLPPYKVICMGIANMRETTILWSRRTG
                                                                                                                                                                                                                                                                                                          614 TALGAAIAANMA 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 NLSTLKYDNELLEFWGIDKNLIHMPEIVSSSQYYGDFGI-----PDWIMEKLHDSPKTVL
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                                                                                                                                                                                                                                                                                                                                                                                                562 FLEEISDVTYEKSPLSVLAVDGGMSRSNEVMQIQADILG-PCVKVRRSPTAEC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 RAPFADPHARAVICGLGMERDLDNLLALYIAGLCGIGYGLRQILDAQT--AQGVVSKN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 LAYVFGTSSCTMASTTSPSFVPGVWGPY---YSAMVPGL----WLVEGGQSAAGAAIDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 RDLVKRNLPIQGCLGDQSASMVGQLAYKPGAAKCTYGTGCFLLYNTGTKKLISQHGALTT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 KWTWLAHENR----WDPD------YFRTIGLAELADEDFIRIGHH------
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                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFSCSKLRWFLDNEPLCTKAYEENDLMFGTVD--TWLIYQLTKQKAFVSDVTNASRTGFM 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAPYWDPDARATIMGMSQFTTASHIARAAVEGVC---FQARAILKAMSSDAFGEGSKDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDFHPAVEEAREMAQRVNQPLPVWLAD--RILEKTAQP---SDAVALAKGLHVVPEFLGN 383
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E: Genencor International, Inc
4 Cambridge Place
                                                                                                                                 GENERCOR INTERNATIONAL,
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21.0%;
                                                                                      METHOD FOR THE RECOMBINANT PRODUCTION OF 1,3 PROPANEDIOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CR-9982
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Pred. No. 4.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 709;
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NAME: Glaister, Debra
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-864-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/U
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: 60/03
FILING DATE: 13-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                           384 RAPFADPHARAVICGLGMERDLDNLLALYIAGLCGIGYGLRQILDAQT--AQGVVSKN--
                                                                                                                                                                          431
                                                                                                                                                                                                                                                                                                                                                     316
505 FAPYWDPDARATIMGMSQFTTASHIARAAVEGVC---FQARAILKAMSSDAFGEGSKDRD
                                                                                                                                                                                                                                                            371 RDLVKRNLPIQGCLGDQSASMVGQLAYKPGAAKCTYGTGCFLLYNTGTKKLISQHGALTT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 EMETPKILWLKENMP---EIYERAGQFFDLADFLTW-----RATGDLARSVCTVTC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 KPI------VNYGIVWNDTRTIKIVRDKWQNTSVDRQLQLRQKTGLPLL------ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 VECHPQKLLVNVVQCLASSLLSLQTINSERVANGLPPYKVICMGIANMRETTILWSRRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 DPLPVSPEGDAKQNIIVWMDHRATE------QAERINATHHPVLNYVGGKISP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 VEQSSQEIWQAVCSCIRNA-LTLADVCAQSVA------GIGFDATCSLVVLDKNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                       --IVSPGTPCGNGLTAQAAAEMGLLPGTPVA-----VGLIDAHAGGIGTVGVEGGALNN 275
                                                                                                                                                                                                                                                                                                                                                     NLSTLKYDNELLEFWGIDKNLIHMPEIVSSSQYYGDFGI-----PDWIMEKLHDSPKTVL
                                                                                                                                                                                                                                                                                                                                                                                            KWTWLAHENR - - - - WDPD - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                           YFSCSKLRWFLDNEPLCTKAYEENDLMFGTVD--TWLIYQLTKQKAFVSDVTNASRTGFM
                                                                                                                             LDFHPAVEEAREMAQRVNQPLPVWLAD--RILEKTAQP---SDAVALAKGLHVVPEFLGN
                                                                                                                                                                                                                   LAYVFGTSSCTMASTTSPSFVPGVWGPY---YSAMVPGL----WLVEGGQSAAGAAIDQL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116; Conservative
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                                                                                    WLRDNLRLIDKSEDVGPIASTVPDSGGVVFVPAFSGL
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· ·	Db 614 TALGAAIAANMA 625 RESULT 13 US-09-297-928-15 Sequence 15, Application US/09297928 Sequence 15, Application US/09297928 Patent No. 6358716 GATEMBY, ANTHONY A. HAYNLE, SHARON L. HAYNLE,
	Qy 477 SAILGAVAGNIA 488
FLEEISDVTYEKSPLSVLAVDGGMSRSNEVMQIQADILG-PCVKVRRSPTAEC 613	Db 562 FLEEISDVTYEKSPLSVLAVE
INTERPROPERTY AND TO STANT THE PROPERTY OF	
TTOOCEPVILG	440

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276 431 431 329 329 505 505 506 614 477 477 614 709-036- Sequence Generation Appli A	189 316 224 371	258 YFSCSKLRWFLDNEPLCTKAY 189 KWTWLAHENRWDPD
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APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawford; Kathryn P
APPLICANT: Trawford; Kathryn P
APPLICANT: Maddurl, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIV1
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT FILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-08-09
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-370-700-5
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09370700 Patent No. 6274350 GENERAL INFORMATION:
                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 4928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 126; Conserv
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ORGANISM: Saccharopolyspora spinosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2451 AAAAGEEQL-RPLLAD-CGDRVGIAAVNAPGSVVLSGDRDVLDDIAGRL 2497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2353 ELDAHLGOMAR-----LRDVLSGSDTQLLDQTLWAQPG-LFALQVGLW---ELLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2191 RRAGVSSFGISGT-NAHLILEQPPRESQRSTEPD-----SGSVRDF-PVVPWMVSGK 2240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2132 -GHTQAAAGVAGVIKMVMAMRQGELPRTLHVDEPSAQVDWSAGTVQLLTENTPWPDSGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2088 DAVEAHGTGTRLGDPIEAQALIATYGRDRDPGRPLWLGSVKSNI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2293 LPGLKALAVSNDAAEVITGTRAAGPVGFVFSGQGGQWPGMGSGLHSAFPVFADAFDEACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 ARS-VCTVTCKWTWLAH------ENRWDPDYFRTIGLAELADEDFIRIGHHIVSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 ATHHPVLNYVGGKISPEM-----ETPKILWLKENMPEIYERAGQFFDLADFLTWRATGDL 179
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 EKITTTRRS------GSRVEQS------SQE--IWQAVCSCIRNALTLADV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGGAGQHPLVRQILADTCGIPVITTQCCEP---VLLGSA-ILGAVAGNI 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGV-----RPAVVLG----HSVGELAAAFAAGVLSLRDAARLVAGRARLMQALPTGGAML 2450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAPFADPHARAVICGLGMERDLDNLLALYIAGLCGIGYGLRQILD-AQTAQGVVSKNIVI 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ASTTSPSFVPGVWGPYYSAMVPGLWLVEGGQ-SAAGAAIDQLLD-FHPAVEEA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIG-TVGVEGGALNNLAYVFGTSSCTM
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δõ 밁 Ş Вb δÃ 뫄 ρ 밁 Qy 밁 QΥ 밁 Qy 멍 δÃ Ъ δÃ US-09-370-700-5 Query Match 3.8%; Best Local Similarity 23.8%; Matches 2241 2132 2400 2353 2191 2451 AAAAGEEQL-RPLLAD-CGDRVGIAAVNAPGSVVLSGDRDVLDDIAGRL 2497 2293 LPGLKALAVSNDAAEVITGTRAAGPVGFVFSGQGGQWPGMGSGLHSAFPVFADAFDEACC 180 2088 DAVEAHGTGTRLGDPIEAQALIATYGRDRDPGRPLWLGSVKSNI-----------2031 ERLSDARRNGHEVLAVVRGSAVNQDGASNGLTAPNGPSQQRVITQALTSA---GLSVSDV 2087 384 339 288 229 34 EKITTTRRS------GSRVEQS------SQE--IWQAVCSCIRNALTLADV 70 TP--EALSAQADALMSYLSNR------VDASPRDIGYSLAVTRPALDHRAVVLGADRAAL WGV-----RPAVVLG----HSVGELAAAFAAGVLSLRDAARLVAGRARLMQALPTGGAML 2450 ----ASTTSPSFVPGVWGPYYSAMVPGLWLVEGGQ-SAAGAAIDQLLD-FHPAVEEA--RRAGVSSFGISGT-NAHLILEQPPRESQRSTEPD-----SGSVRDF-PVVPWMVSGK 2240 ARS-VCTVTCKWTWLAH------ENRWDPDYFRTIGLAELADEDFIRIGHHIVSPG 228 ATHHPVLNYVGGKISPEM-----ETPKILWLKENMPEIYERAGQFFDLADFLTWRATGDL 179 CAQSVAGIG-----FDATCSLVVLDKNGDPLPVSPEGDAKQNIIVWMDHRATEQAERIN 124 SGGAGQHPLVRQILADTCGIPVITTQCCEP---VLLGSA-ILGAVAGNI ELDAHLGQMAR-----LRDVLSGSDTQLLDQTLWAQPG-LFALQVGLW---ELLGS TPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIG-TVGVEGGALNNLAYVFGTSSCTM RAPFADPHARAVICGLGMERDLDNLLALYIAGLCGIGYGLRQILD-AQTAQGVVSKNIVI 442 -GHTQAAAGVAGVIKMVMAMRQGELPRTLHVDEPSAQVDWSAGTVQLLTENTPWPDSGRL 2190 126; -----REMAQRVNQPLPVWLAD-----RILEKT--AQPSDAVALAKGLHVVPEFLGN 383 Conservative 65; Mismatches Score 106.5; 1 Pred. No. 1.7; DB 4; 201; Indels 137; Length 4928; 487 Gaps 2352 338 2399 2292 287 31;

Search completed: March 13, 2003, 16:42:17 Job time: 21.5877 secs

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Listing first 45 summaries
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: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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10 US-09-738-626-6686

10 US-09-815-242-13431

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Sequence 11837, A
Sequence 12837, A
Sequence 5796, Ap
Sequence 6686, Ap
Sequence 10425, A
Sequence 13431, A
Sequence 13660, A
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                                              Sequence 1335, A Sequence 1335, A Sequence 13788, A Sequence 11927, A Sequence 10714, A
             Sequence 3630, Ap
Sequence 11747, A
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Sequence 10383, A
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Publication No. US20030041352A1
GENERAL INFORMATION: |
APPLICANT: Parrott, Wayne
APPLICANT: LaFayette, Peter
APPLICANT: Kane, Patrick
TITLE OF INVENTION: Arabitol or Ribitol As Positive Selectable
FILE REFERENCE: UGA-855R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/802,208B CURRENT FILING DATE: 2001-03-08 NUMBER OF SEQ ID NOS: 5
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US-09-900-237-30	US-10-051-909-37	US-09-955-909-2	US-09-900-237-20	US-09-976-059-15	US-09-712-363-261	US-09-815-242-10786	US-09-996-194-6	US-09-900-237-32	US-09-861-289-6	US-09-860-846-6	US-09-861-289-33	US-09-860-846-33	US-09-738-626-5603	US-09-838-539-8	US-09-287-849-2	US-09-738-626-4295	US-09-815-242-12027	US-09-738-626-6239	US-09-815-242-13341	US-09-764-847-580	US-10-176-640-3	US-09-820-843A-60	US-09-833-745-63	US-10-001-852-12	US-09-308-207-18
	Sequence 37, Appl	Sequence 2, Appli	Sequence 20, Appl	Sequence 15, Appl	Sequence 261, App	Sequence 10786, A	Sequence 6, Appli	Sequence 32, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 33, Appl	Sequence 33, Appl	Sequence 5603, Ap	Sequence 8, Appli	Sequence 2, Appli	Sequence 4295, Ap	Sequence 12027, A	Sequence 6239, Ap	Sequence 13341, A	Sequence 580, App	Sequence 3, Appli	Sequence 60, Appl	Sequence 63, Appl	Sequence 12, Appl	Sequence 18, Appl

ALIGNMENTS

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US-09-802-208B-4
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Matches
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TYPE: PRT
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                                                    RSVCTVTCKWTWLAHENRWDPDYFRTIGLAELADEDFIRIGHHIVSPGTPCGNGLTAQAA
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100.0%; Pred. No. 7.1e-251;
tive 0; Mismatches 0;
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US-09-815-242-10383
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version SEQ ID NO 10383
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                                                                                                                                                                                                                         Matches
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APPLICANT:
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TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                          HSLQDVKALGIAGQMHGATLL------DAQQRVLRPAILWNDGRCAQEC 105
                                                                                               LTLADVCAQSVAGIGFDATCSLVVLDKNGDPLPVSPEGDAKQNI----IVWMDHRATEQA 120
                                                                                                                                        IGIDLGTSGVKVILLNEQGEVVAAQTEKLTVSRPHPLWSEQDPEQWWQATDRAMKALGDQ
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Pred. No. 6.1e-20;
'5; Mismatches 249;
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                                                          ; ORGANISM: Enterococcus
US-09-815-242-10866
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                                                                                                                                      SOFTWARE: Fast
SEQ ID NO 10866
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/257,931
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                  CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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APPLICANT:
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TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
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Yamamoto, Robert T.
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US-09-815-242-11080
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US-09-815-242-12837
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                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            Sequence 12837, Application US/09815242 Patent No. US2002006[1569A1
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Best Local Similarity
TITLE OF INVENTION: Identification of ESS
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                  Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                      Carr, Grant J.
                                                                                                                                                            Trawick, John D.
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Zyskind, Judith W.
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                                                                                  Essential Genes
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 12837
LENGTH: 517
                                                          RESULT 6
US-09-815-242-5796
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; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12837
               Sequence 5796, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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Best Local
   APPLICANT: Haselbeck,
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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                                                                                                                                                     YYPQERYQSLHHRRYEAYKQL-----QHTAK 530
                                                                                                                                                                                   MMSDIFDTELVVPESYESSCLGACVLGLKAVGDIEDFSIVSSMVGATNNHTPIEENVTVY
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Pred. No. 2.5e-18;
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Matches 122
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SEQ ID NO 5796
LENGTH: 509
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; ORGANISM: Staphylococcus aureus US-09-815-242-5796
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CURRENT FILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                          IDKPRTDYQGRIFCYVLAEDHYVIG--GPVNNGGVVLRWL-----RDELL--AS
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ROMMSDIFDTELVVPESYESSCLGACVLGLKAVGDI
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                                                                                                   GSFFGLTLSHKKEHMIR----AALEGVLYNLYTVYLALIEVMNETPKMIKATGGFAKSEVW
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Pred. No. 3e-18;
Prematches 221;
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SEQ ID NO 66886
LENGTH: 509
TYPE: PRT
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PRIOR FILING DATE: 2000-04-07
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PRIOR FILING DATE: 1999-12-16
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                                                                                         LGNRAPFADPHARAVICGLGMERDLDNLLALYIAGLCGIGYGLRQILDAQTAQ-GVVSKN 439
                                                                                                                                LRDNLQLIPNAPAIENLAREVEDN-
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                                                     TGLFAPRWRPDARGVITGL---TRFANRKHIARAVLEANAFQTREVVDAMAKDAGKALES
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OZAKI, AKIO
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TATEISHI, NAOKO
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Pred. No. 1.8
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US-09-815-242-10425
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LENGTH: 502
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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  288 ASTTSPSFVPG<sub>|</sub>---
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mes 129; Conserv
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                                                                                     PCGNGLTAQAAAEMGLLPGTPVAVGLI---DAHAGGIGTVGVEGGALNNLAYVFGTSSCTM
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                                            -----GTRIPISGIAGDQQAALFGQLCVKEGMAKN---TYGT-GCFM
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--VWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLDFHPAVEEAR 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 276.5; DB 10;
Pred. No. 3.4e-17;
8; Mismatches 251;
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                                                                                                                                                                                                                               ; TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13431
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                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13431, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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                                                                              61
                                                                                                                        FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23 APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27 APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
   AERINATHHPVLNYV-----GGKISPEMETPKILWLKENMPEIYERAGQ----FFDLA 168
                                                                      IRNALTLADVCAQSVAGIGE-DATCSLVVLDKNGDPLPVSPEGDAKQNIIVWMDHRATEQ 119
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                                             IAGAFIESGVKPNQIEAIGITNQRETTVVWDKK-TGLPI-----YNAIVWQSRQTAPL 112
                                                                                                        MSQEKYIMAIDQGTTSSRAIIFNKKGEKVSSSQKEFTQIFPQAGWVEHNANEIWNSVQSV
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                                                                                                                                                                                Score 276.5; DB 10; Pred. No. 3.4e-17;
                                                                                                                                                                    Mismatches
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Local Similarity
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; ORGANISM: Streptococcus pneumoniae US-09-815-242-13660
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: Sequence 13660, Application US/09815242
: Patent No. US20020061569A1
                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13660 LENGTH: 502
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
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Zyskind, Judith W.
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9.7%;
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  Score 273.5; DB 10; Pred. No. 6.4e-17;
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RESULT 11
US-10-116-821-14
; Sequence 14, Application US/10116821
; Publication No. US20030040086A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                SEQ ID NO 14
TENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/116,821
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/282,277
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Methods for the Production TITLE OF INVENTION: in Host Cells FILE REFERENCE: GC620-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dodge, Timothy C. APPLICANT: Valle, Fernando
                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                         ORGANISM: Pantoea
                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 GELFEPSMNESRKEQLYKGWKKAVKATQVFAEV 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 VEEAREMAORVNOPLPVWLADRILEKTAOPS----DAVALAKGLHVVPEFLGNRAPFADPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 IMNTGEEMQLSENNLLTTIGY--GINGKVYYAL-----EGSIFIAGSAIQWLRDGLRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 -----GKTAPFHFYGGEVPISGMAG---DQQAALFGQLAFEPGMVKN---TYGTGSFI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 AEQLKNQ-----GYVEKFHEKTGLIIDAYFSATKVRWILDHVEGAQERAEKGELLFGTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 DFLTWRATGDLARSVCTVTCKWTWLAH--ENRWDPDYFRTIGLAELADEDFIRIGHHIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 AERINATHHPVLNYV-----GGKISPEMETPKILWLKENMPEIYERAGQ----FFDLA
                                                                                                      Local Si
hes 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQHPLVRQILADTCGIPVITTQCCEPVLLGSAILGAVAGNIAPSVG-----EAMQQFTHV
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                                           KTVIGVDVGSGSVRAGIFDLNGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKYYYP---QERYQSLHHRRYEAYKQLQHTAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARGSVFGLTRGTSKEDFIK---ATLQSIAYQVRDIIDTMQVDTQTAIQVLK----VDGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARAVICGLGMERDLDNLLALYIAGLCGIGYGLRQIL-----DAQTAQGVVSKNIVISGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSQEKYIMAIDQGTTSSRAIIFNKKGEKVSSSQKEFTQIFPQAGWVEHNANEIWNSVQSV
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                     KYIVALDQGTTSSRAVVLDHDANIIAVSQREFTQHYPKTGWVEHDPMDIWATQSSTLVEV 66
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                                                                                                    Score 267.5; DB 9;
Pred. No. 2.3e-16;
O; Mismatches 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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US-09-815-242-5321
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ, for Windows Version
SEQ ID NO 5321
LENGTH: 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5321, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Esse
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 50/191,078
PRIOR APPLICATION NUMBER: 50/191,078
                                                                              PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                         PRIOR EILING DATE: 2000-10-23
                                                                                                                                                                                                                                                  PRIOR EILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                            FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/
FILING DATE: 2000-05-23
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| KK 491
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489

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TITLE OF INVENTION: INCREASE
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION UMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/21,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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APPLICANT:
APPLICANT:
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Matches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395 VICGLGMERDLDNLLALYIAGLCGIGYGLRQILDAQTA-QGVVSKNIVISGGAGQHPLVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEVPIAGVAGDQQAALFGQACFERGDVKNTYGTGGFMLMNTGD-KAVKSESGLLTTIAY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKQQGYEQTFRDKTGLLLDPYFAGTKVKWILDNVEGAREKAENGDLLFGTIDTWLVWKLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INENDVRADQIAGIGITNQRETTVVWDKHTGRPI-----YHAIVWQSRQTQSICSE
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                                                                                                                                                                                                                                                                                                              Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                      Trawick, John D. Carr, Grant J.
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Zyskind, Judith W.
Wall, Daniel
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milarity 21.98;
Conservative 7
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; Pred. No. 4.2e-16;
77; Mismatches 227; Indels
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Sequence 13788, Application Patent No. US20020061569A1 GENERAL INFORMATION:

US/09815242

APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W APPLICANT: Wall, Daniel

Ohlsen, Kari L. Zyskind, Judith Wall, Daniel

APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Ess.
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR ADDITORATION NUMBER: US/09/815,242

Essential

Genes

PRIOR PRIOR

APPLICATION NUMBER: 60/191,078 FILING DATE: 2000-03-21

APPLICANT:

Carr, Grant J. Trawick, John D.

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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEO ID NOS: 14110
SOFTWARE: FastSEO for Windows Version 4
SEQ ID NO 12335
LENGTH: 498
RESULT 14
US-09-815-242-13788
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                                                               QFQADIVNTSVERPEIQETTALGAAYLAGLA
                                                                                               QILADTCGIPVITTQCCEPVLLGSAILGAVA
                                                                                                                                                                                                                                                                                         FGTSSCTMASTTSPSFVPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLDFHPAVEEAR 339
                                                                                                                                                                                                                                                                                                                                                                                          GKAAHITDYSNASRTLMFNIHDLEWDDELLELLTVPKNMLPEVKPSSEVYGKTIDYHFYG
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                                                                                                                               AIFGLTRGTEKEHFIRATLESLC---YQTRDVMEAMSKDSGIDVQSLRVDGGAVKNNFIM
                                                                                                                                                                                                                          EMAQRVNQPLPVWLADRI-LEKTAQPSDAVAL----AKGLHVVPEFLGNRAPFADPHARA 394
                                                                                                                                                                                                                                                                                                                          QEVPTAGVAGDQQAALFGQACFERGDVKNTYGTGGFMLMNTGD-KAVKSESGLLTTIAY-
                                                                                                                                                                                                                                                                                                                                                          PGTPCGN-----GLTAQAAAEMGLLPGTPVAVGLIDAHAGGIGTVGVEGGALNNLAYV
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21'.9%;
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APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
FILING DATE: 2000-10-23

FILING DATE:

APPLICATION NUMBER: 60/206,848

2000-05-23

APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27 APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22

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LOCATION: (1)...(501)
: OTHER INFORMATION: Xaa =
US-09-815-242-13788
RESULT 15
US-09-815-242-11927
; Sequence 11927, Application US/09815242
; Patent No. US20020061569A1
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Best Local Similarity
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 13788
LENGTH: 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                     484 SGWKK 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 LKRDXLEDYIRDNTGLVVDPYFSGTKVKWILDHVEGSRERAKRGELLFGTVDTWLIWKMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 I--NATHHPVLNYVGGKISPEMETPKILWLKENMPEIYERAGQ----FFDLADFLTWRAT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 LAKADISSDQIAAIGITNQRETAIVWERETGKPI-----YNAIVWQCRRTANICEQ
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                                                                                                                                                                                                                                                                                                                                                         ----YFATKVKD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTAQAAAEMGLLPGTPVAVGLI--DAHAGGIGTVGVEGGALNNLAYVFGTSSCTMASTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGRVHVTXYTNASRTMLFNIHDLDWDDKMLDVLDIPR-AMLPQVRKSSEVYGQTNIGGKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTLADVCAQSVAGIGF -- DATCSLVVLDKNGDPLPVSPEGDAKQNIIVWMDHRATEQAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYIVALDQGTTSSRAVVMDHDANIVSVSQREFEQIYPKPGWVEHDPMEIWASQSSTLVEV
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                                                                                                                                                                                                                                                                             SNHIIR---ATLESIAYQTRDVLEAMQADSGIRLHALRVDGGAVANNFLMQFQSDILGTR 429
                                                                                                                                                                                                VERPEVREVTALGAAYLAGLAVGYWQNLDE-LQEKAVIEREFRPGIETTER---
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US-09-815-242-11927
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Best Local S
Matches 120
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: | 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
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les 120; Conserv
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APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                             LTAQAAAEMGLLPG--TPVAVGLIDAHAGGIGTVGVEGGALNNLAYVFGTSSCTMASTTS
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Zyskind, Judith W.
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                                                                                                                     ---SNGVYLVPAFTGLGAPYWDPYARGAVFGLTRGVKADH
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Search completed: March 13, 2003, 16:51:23 Job time : 17.0298 secs B 437 PVMRETTALGAAYLAGLACGFWSSLDE-LKSKAVIERVFEPE 477

ise: PIR_73:*

1: pir1:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	Ç	4	ω	2	1	No.	Result	
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244 GLLPGTPVAVGLIDAHAGGIGTVGVEGGALNNLAYVFGTSSCTMASTTSPSFVPGVWGPY 303

C. Land or Victorian

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244 61156	184 CTVTCI 185 CTVTCI	124 NATHH 125 NATGH	64 ALTLADVCAQ : 65 AVANAGVSPS	4 TKTVI	latch cal (A; Gene: rock C; Function: A; Description: catalyzes ph C; Superfamily: ribulokinase C; Keywords: phosphotransfer	cule type dues: 1-1 erimental :	Reference number: S07,135; MUID:86050; Accession: S08571	Cross-references: EMBL:AF045; Experimental source: strain I; Loviny, T.; Norton, P.M.; Has lochem. J. 230, 579-585, 1985 Title: Ribitol debydrogenase	ssion: S7	ted to the preparation: Shiption: (1 lokinase les: Kleb		325 324 322 323 322.5 322.5 321.5 319.5 319.5 316.5 316.5 316.5 316.5 317.5
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meneruncianony 202	PCGNGLTAQAAAEM 243 PCGEGLCATAAEEM 244	ELTWRATGDLARSV 183 : : ' !LTWRSTGDEARSV 184	VWMDHRATEQAERI 123 - VWMDHRATGQAEKI 124	SQEIWQAVCSCIRN 63 : : SREIWQAVCYCIKT 64	Length 535; Indels 0; Gaps 0;	o D-ribulose-5-phosphate		education of error	Sequence of the structural		J.W. lism in enteric bacteria.	text_change 17-mar-2000		xylulokinase (EC 2 glycerol kinase - sugar kinase homol xylulose kinase xy probable L-xylulok glycerol kinase (E gluconate kinase h cryptic L-xylulose probable carbohydr ATP-stimulated glu sugar kinase, FGGY probable xylulose L-xylulose kinase probable xylulose transporter/facili glycerol kinase (E

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RESULT 2
A99199
D-ribulokinase (EC 2.7.1.47) [imported] -
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-
C:Accession: A99199
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A;Gene: AGR_L_1075
A;Map position: linear chromosome
C;Superfamily: ribulokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2386, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrot A;Reference number: A97359; PMID:11743194
A;Accession: A99199
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A; Residues: 1-536 < KUR>
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                                                                                                                                                                 TCKWTWLAHENRWDPDYFRTIGLAELADEDFIRIGHHIVSPGTPCGNGLTAQAAAEMGLL 246
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  AVKLAEDFHMVPEFLGNRAPFADPHARAIIAGYGMETGVDSLVALYVAGLLGLGYGLRQI
                                                   MVPGAWLNEGGQSAAGAAIDYLVQLHPAFAEAKALADKDGKALPVWLADRALSLAASASA
                                                                                                   AGTAVAAGLIDAHAGGVGTVAAGGDASRCLGYVFGTSSCTMTTTTEPAFVPGVWGPYYSA
                                                                                                               PGTPVAVGLIDAHAGGIGTVGVEGGALNNLAYVFGTSSCTMASTTSPSFVPGVWGPYYSA
                                                                                                                                                                                                                            HHPVLNYVGGKISPEMETPKILWLKENMPEIYERAGQFFDLADFLTWRATGDLARSVCTV 186
                                                                                                                                                                                                                                                       RAGIDPAEVTGIGFDATCSLVVRGPGDVTLPVGAADHPERDIIVWMDHRAVEQAERINAG
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                                                                                                                                                                                                                                                                                                                                                                    Score 1666; DB 2; Pred. No. 4.9e-117;
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                                                                                                                                                                                                                                                                                                                                                         Mismatches 146;
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Markelz,
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kelz, B.;
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A;Experimental source: strain C58
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-536 <KUR>
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Best Local Similarity
Matches 316; Conserv
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IAPSVGEAMQQFTHVDKYYYPQERYQSLHHRRYEAYKQLQHTAKLLR 533
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl; Karp, P.; Romero, P.; Zhang; S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The Genome of the Natural Genetic A;Reference number: AB2577; PMID:11743193 A;Accession: AH3087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 VIGVDVGSGSVRAGIFDLNGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNALT
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5 LVGVDVGTGSARAGVEDVAGKLLATAKRPISMHREDGGIAEQSSAEVWQAVCDSVRDSVS
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                                                                                                                                 AVALAKGLHVVPEFLGNRAPFADPHARAVICGLGMERDLDNLLALYIAGLCGIGYGLRQI
                                                                                                                                                                                                                                           MVPGLWLVEGGQSAAGAAIDQLLDFHPAVEEAREMAQRVNQPLPVWLADRILEKTAQPSD
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                                                                                                         AVKLAEDFHMVPEFLGNRAPFADPHARAIIAGYGMETGVDSLVALYVAGLLGLGYGLRQI
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IETQARNGAPVETISVSGGAGAHPLARQLLADATGLPVELTECEEPVLLGSAMLGAVAAG
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A; Experimental source: strain 1
C; Genetics:
A; Gene: BMEII0979
A; Map position: II
C; Superfamily: ribulokinase
C; Keywords: phosphotransferase
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688

A;Rocession: AB3632

A;Status: preliminary
A;Molecule type: The second sequence of the facultative intracellular pathogen Brucella melitens A;Accession: AB3632

A;Status: preliminary
A;Molecule type: The second sequence of the facultative intracellular pathogen Brucella melitens A;Accession: AB3632
                                                           RESULT 5
AF0442
probable carbohydrate kinase YPO3637 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AF0442
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AB3632
D-ribulokinase (EC 2.7.1.47) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 17-May-2002
C;Accession: AB3632
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A; Residues: 1-538 < KUR>
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;Superfamily: ribulokinase
;Keywords: phosphotransferase
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Best Local
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Pred. No. 4e-109
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                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-569 <ST(
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C;Genetics:
A;Gene: YPO3637
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A; Residues: 1-545 < KUR>
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                                                           <STO>
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A; Title: Genome sequence of Yersinia pestis, the causative A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Traga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, I.M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 IGVDVGSGSVRAGIFDLNGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNALTL
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                                        SAILGAVAGNIAPSVGEAMQQFTHVDKYYYPQ-ERYQSLHHRRYEAYKQLQH
                                                                                                   QALALGTRHIIETMNQNGYNIDTMMASGGGTKNPIFVQEHANATGCAMLLPEESEAMLLG
                                                                                                                                                                                                                                                                                                          PYYSAILPEYWLNEGGQSATGALIDHIIQSHPCYPALLEQAKNKGETIYEAL-----NYI
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SAMMGTVAAGVFESLPEAMAAMSRIGKTVTPQTNKIKAYYDRKYRVFHQMYH
                                                                                                                                                 CGIGYGLRQILDAQTAQGVVSKNIVISGGAGQHPLVRQILADTCGIPVITTQCCEPVLLG
                                                                                                                                                                                                         LRQMAGEPENIAFLTNDIHMLPYFHGNRSPRANPNLTGIITGLKLSTTPEDMALRYLATI
                                                                                                                                                                                                                                    LEKTA-QPSDAVALAKGLHVVPEFLGNRAPFADPHARAVICGLGMERDLDNLLALYIAGL
                                                                                                                                                                                                                                                                                                                                       PYYSAMVPGLWLVEGGQSAAGAAIDQLLDFHPA----VEEAREMAQRVNQPLPVWLADRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CKWTYLGHEDRWDPSYFKLVGLADLLDNNAAKIGATVKPMGAPLGHGLSQRAASEMGLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPVLEFVGGVISPEMQTPKLLWLKQHMPNTWSNVGHLFDLPDFLTWRATKDETRSLCSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADINPIQVKGLGFDATCSLVVLDKEGNPLTVSPSGRNEQNVIVWMDHRAITQAERINATK
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Pred. No. 2e-85;
0; Mismatches 1
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hypothetical protein AT4q30310 [imported] - Arabidopsis thaliana (c;Species: Arabidopsis thaliana (mouse-ear cress) (;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change :C;Accession: D85354 (;Accession: The European Union Arabidopsis Genome Sequencing Construct 402, 769-777, 1999 A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A; Reference number: A\$5001; MUID:20083488; PMID:10617198 GB:NC_001268; NID:g7269931; PIDN: CAB81024.1; Sequencing Consortium, #text_change 16-Feb-2001 GSPDB: GN00140 The Cold

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D-ribulokinase (EC 2.7.1.47) [imported] - Agrobacte C:Species: Agrobacterium tumefaciens C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 C:Accession: A96183 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D. Science 294, 2323-2328, 2001
                                                                                                                                                     A;Gene: AGR_L_826
A;Map position: 1
C;Keywords: phosp
                                                                                                                                                                                                                                                                                                                           A; Reference number: A97359; A; Accession: A96183
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A96183
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                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-525 <KUR>
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Best Local Sim
Matches 216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKWTYLGHAHMHQMTEKASRDMEACGWDDEFWEEIGLGDLVDGHHAKIGRSVAFPGHPLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILPRESESVLLGAAILGAVAGKNYPSLHDAMKALNAAGQVVHPSSDPKIKKYHDAKYRIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITTQCCEPVLLGSAILGAVAGNIAPSVGEAMQQFTHVDKYYYPQE--RYQSLHHRRYEAY
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                                                               Score 971; DB 2; L
Pred. No. 6.1e-65;
91; Mismatches 187;
                                                                                                                                                                                                                                           PIDN: AAK88987.1;
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Pred. No. 1.3e-79;
Pred. Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -WDPDYFRTIGLAELADEDFIRIGHHIVSPGTPCG
                                                                                                                                                                                                                                                                                                                                                                                                            Miller, N.; Blanchard, M.; Qurollo, Doughty, D.; Scott, C.; Lappas, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobacterium tumefaciens (strain
                                                                                                                                                                                                                                         PID:g15158771; GSPDB:GN00170
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Markelz,
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                                                                                          LTLADVCAQSVAGIGFDATCSLVVLDKNGDPLPVSPEGDAKQNIIVWMDHRATEQAERIN
                                                                                                                                                     QNLVAVDVGTASARAGIFDPAGRLLARSIHPILMQRPRENHAEHDSTDIWNAVCIAVKAA
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                      ATHHPVLNYVGGKISPEMETPKILWLKENMPETYERAGQFFDLADFLTWRATGDLARSVC
                                                                    LADAGVLPQSIAAIGFDATCSLVIRDERGEPVSVSTTDDDRFDTIVWLDHRAIGEADRLT
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11-Jan-2002 #text_change 11-Jan-2002

(strain C58,

Dupont)

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                                                                                                                                     GLCGIGYGLRQILDAQTAQGVVSKNIVISGGAGQHPLVRQILADTCGIPVITTQCCEPVL
                                                                                                                                                                                                                                     DRILEKTAQPSDAVALAKGLHVVPEFLGNRAPFADPHARAVICGLGMERDLDNLLALYIA 414
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LGTAMTAATAGGVHASLAAAGAAMYPGNAEISGNPALAAHYERDY---RRFLAMYRHRQE
                                                                                                                                                                                                           ARVTE--LRELEGEAFADRLHVLPDFHGNRSPLADPHAVGVVSGLTLDTSFDSLCRLYWR
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A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-525 < KUR>
A;Cross-references: GB:AE008689; A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; PMID:11743193 A; Accession: AI3103 A; Authors: Yoo, H.; Tao, Y.; Biddle, KTVIGVDVGSGSVRAGIFDLNGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNA linear chromosome 34.5%; C58 91; PIDN: AAL45247.1; Score 971; DB 2; Pred. No. 6.1e-65; 1; Mismatches 187; (Dupont) P.; Jung, Engineer D.; Chen, M.; Krespan, .; Chen, L.; Kutyavin, T PID:g17742931; Agrobacterium Length 525 Indels Σ. wood, od, G.E.; Chen, Levy, R.; Li, 46; Perry, GSPDB:GN00187 tumefaciens C58 Gaps 64 M.; Gordon-Kam 13; м` ч.: MCC1

123 124 63

184

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probable membrane protein YDR109c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YD9727.05c
C;Species: Saccharomyces cerevisiae
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: $52675
R;Murphy, L.; Shore, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: $52671
A;Accession: $52675
A;Molecule type: DNA
A;Residues: 1-715 <MUR>
A;Cross-references: EMBL:Z48758; NID:g747879; PID:g747884; GSPDB:GN00004; MIPS:YDR109c
C;Genetics:
A;Gene: MIPS:YDR109c
A;Cross-references: SGD:S0002516
A;Map position: 4R
C;Reywords: transmembrane protein
F;515-531/Domain: transmembrane #status predicted <TM1>
F;535-551/Domain: transmembrane #status predicted <TM2>
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                                                                              GNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIGTVGVE-----
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                             ISPLDKKAACQLGLTEHCVVSSGIIDAYAGWVGTVAAKPESAVKGLAETENYKKDFNGAI
                                                                                                                                 FCSAVCKQGFLPVGVEGSDIGWSKEFLNSIGLSELTKNDFERLGGSLREKKNFLTAG-EC
                                                                                                                                                                                     VCTVTCKWTWL----AHENRWDPDYFRTIGLAELADEDFIRIG-----HHIVSPGTPC
                                                                                                                                                                                                                                     INSSGDKCLKYVGGQMSVEMEIPKIKWLKNNLEAGIFQDCKFFDLPDYLTFKATGKENRS
                                                                                                                                                                                                                                                                                                                                            VEESGVDPERVRGIGFDATCSLVVVSATNFEEIAVGPDFTNNDQNIILWMDHRAMKETEE
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A.Experimental source: strain 1021, megaplasmid pSymB
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A;Title: The complete sequence of the 1.683-kb psymB megaplasmid from the N2-fixing A;Reference number: A95842; MUID:21396508; PMID:11481431
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A; Residues: 1-509 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Genome: plasmid
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                                                                                                                                                                                                                                                                                            64 AKAGSPDIAAVCVATF----ASTVVLCDRSGK--PIAP-----AVLWMDARAADEAAF
                                                                                                                                                                                                                                                                                                                                                                                                4 VLSLDFGTGGARAAIFDTQTNHIVARGEAPYKTQHLPPNRAEQNPEDWMTALVSLVPDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                              7 VIGVDVGSGSVRAGIFDL-NGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNAL
INATHHPVLNYVGGKISPEMETPKILMLKENMPEIYERAGQFFDLADFLTWRATGDLARS
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                                                                              LMNATCKWNYDSRNRKFCEDLYALFGVPDLGAKLPQRIVDIG-DVVAPMLP-----EM
                                                                                                                                 VCTVTCKWTWLAHENRWDPDYFRTIGLAELA---DEDFIRIGHHIVSPGTPCGNGLTAQA
                                                                                                                                                                                     TETVDHPILADSGGSDAVEWLVPKAMWFARRKPDLWARTEVICEALDFVNHRLTGVWAGS
                                                                                                                                                                                                                                                                                                                                         TLA----DVCAQSVAGIGFDATCSLVVLDKNGDPLPVSPEGDAKQNIIVWMDHRATEQAER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.5%; Score 465; DB 2;
26.3%; Pred. No. 5.2e-27;
Live 89; Mismatches 213;
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:	OY 228 GTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIGTVGV-EGGALNNLAYVFGTSSCT 286	Db 185 DWIVYQLCGSLKRSNCTAGYKAMWSEKAGYPSDDFFEKLNPSMKTITKDKLSGSIHSV 242	113 DHRALEVARIN''''''''''''''''''''''''''''''''''''	56 AVCSCIRNALTLADVCAQSVAGIGFDAY-CSLVVLDKNODPLPVSPEGDAKQVIIVWM :	u œ	Query Match 16.0%; Score 448.5; DB 2; Length 560; Best Local Similarity 27.1%; Pred. No. 1e-25; Matches 153; Conservative 95; Mismatches 237; Indels 79; Gaps 20;	A;Gene: arab C;Superfamily: ribulokinase	A; Residues: 1-560 < KUN> A; Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14839.1; PID:g2635344 A; Experimental source: strain 168	A;Accession: D09387 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA	A;Authors: Yoshikawa, H.F.; Zumselo, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Reference number: A69580; MUID:98044033; PMID:9384377	A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Seklyuchi, J.; Sekowska, A.; Seron akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, B.; Udati, B.; Tognoni, A.; Tosato, V.; Uchiyama, B.; Udati, B.; Tognoni, A.; Tognoni,	A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteteild Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sarto, T.; Scanlon,	A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,	C.V.; Caldwell, B.; Capuano, V.; Carter, N.» tian, K.D.; Errington, J.; Fabret, C.; Ferrar	text_change	D69587 L-ribulokinase araB - Bacillus subtilis	RESCITOT 11	OY 470 CEPVLLGSAILGAVAGNTAPSVGEA 494 : : Db 431 DNLSLHGGAVACTVALGLFPDLTTA 455	OY 410 ALYIAGLCGIGYGLRQILDAQTAQGVVSKNIVISGGAGQHPLVRQILADTCGIPVITTQC 469	QY 358LEKTAQPSDAVAL-AKGLHVVPEFLGNRAPFADPHARAVICGLGMERDLDNLL 409 : : : :	QY 298 GVWGPYYSAMVPGLWLYEGGQSAAGAAIDQLLDFHPAVEEAREMAQRYNQPLPVWLADRI 357	223 ACTLG-IPGNPVVVQGGIDAHMGTFGADAVTPGSMLFIGGTSNVHLTQVPDDGRNIR
	319 SAAGAAIDQLLDFHPAVEEAREMAQRVNQPLPWLADRILEKTAQ	OY 263 IGTVGVEGGALNNLAYVFGTSSCTMASTTSPSFVPGVWGPYYSAMVPGLWLVEGGQ 318	QY 211 ELADEDFIRIGHHIVSP,GTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGG 262 Db 221 SFFDELDPILNRHLPSPLFTDFWTADIPVGT-LCPEWAQRLGLPESVVISGGAFDCHMGA 279	QY 158 YERAGQEFDLADELTWRATGDLARSVCTVTCKWTWLAHENRWDDDYFRTIGLA 210 :	105 KONIIVWMDHRATEQAERINATHHPVLNYVGGKISPEMETPKILWLKENMPEI 	66TLADVCAQSVAGIGFDATCSL-VVLDKNGDPLPVSPEGDA	QY 8 IGVDVGSGSVRAGIFDLNGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNAL 65	Query Match 14.4%; Score 405.5; DB 2; Length 566; Best Local Similarity 27.7%; Pred. No. 1.7e-22; Matches 163; Conservative 77; Mismatches 224; Indels 125; Gaps 29;	A; dene: ECsU067 C; Superfamily: ribulokinase	A;Residues: 1-365 <hay> A;Residues: 1-365 <hay> A;Cross-references: GB:BA000007; PIDN:BAB33490.1; PID:g13359523; GSPDB:GN00154 A;Experimental source: strain,O157:H7, substrain RIMD 0509952 C;Genetics:</hay></hay>	A; Status; pretiminary A; Molecule type: DNA	omp Omp	R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001	nerichia coli -2001 #sequence_revision 90637	RESULT 12	Db 510 TYTPNAENAAVYEKLYAEVKELVH 533	Oy 504 YYYPQERYQSLHHRRYEAYKQLQH 527	Qy 455 ILADTCGIPVITTQCCEPVLLGSAILGAVAGNIAPSVGEAMQQFTHVDK 503	Qy 396 ICGLGMERDLDNLLALYIAGLCGIGYGLRQILDAQTAQGVVSKNIVISGG-AGQHPLVRQ 454 : : : : ::	Qy 341MAQRVNQPLPVWLADRILEKTAQPSDAVALAKGLHVVPEELGNRAPFADPHARAV 395	QY 287 MASTTSPSEVPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLDFHPAV-EEARE 340 :	GEKAGS-LTEKMAKLTGLLPGTAVAVANVDAHV-SVPAVGITEPGKMLMIMGTSTCH

F.;

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A;Molecule type: DNA
A;Residues: 1-566 <STO>
A;Cross-references: GB:AE005174; NID:g12512760; PIDN:AAG54367.1; GSPDB:GN00145;
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetical A;Gene: araB
C;Superfamily: ribulokinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQN--IIVWMDHRATEQAERINATHHPVLN-----YVGGKISPEMETPKILWLKENMPEI 157
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                                      PSDAVALAKGLHVVPE-FLGNRAPFADPHARAVICGLGMERDLDNLLALYIAGLCGIGYG
                                                                                SAFGDIYAWFGRVLGWPLEQLAAQHPELKEQIDASQK--QLLPALTEAWAKNPSLDH---
                                                                                                                                                               VGA----GAQPNALVKVIGTSTCDILIADKQSVGERAVKGICGQVDGSVVPGFIGLEAGQ
                                                                                                                                                                                                       IGTVGVEGGALNNLAYVFGTSSCTMASTTSPSF----VPGVWGPYYSAMVPGLWLVEGGQ
                                                                                                                                                                                                                                               SFFDELDPILNRHLPSPLFTDTWTADIPVGT-LCPEWAQRLGLPESVVISGGAFDCHMGA
                                                                                                                                                                                                                                                                                        ELADEDFIRIGHHIVSP-----GTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGG
                                                                                                                                                                                                                                                                                                                              AQSAASWIELCDWVPALLSGTTRPQDIRRGRCSAGHKSLW--HES-WG-----GLPPA
                                                                                                                                                                                                                                                                                                                                                                                                            NPNAMFVLWKDHTAVEEAEEITRLCHAPGNVDYSRYIGGIYSSEWFWAKILHVTRQDSAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILGAVAGNIAPSVGEAMOOF-THVDKYYYPQ----ERYQSLHHRRYEAY 522
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  -LPVVLDWFNGRRTPNANQRLKGVITDLNLATDAPLLFGGLIA---ATAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TLADVCAQ---SVAGIGFDATCSL-VVLDKNGDPLPVSPEGDA 104
                                                                                                                      ---AGAAIDQLLDFHPAVEEAREMAQRVNQPLP----VWLADRILEKTAQ
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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000
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A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A; Reference number: A83650; MUID:20512582; PMID:11058132

A; A; Accession: H83883
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A;Molecule type: DNA
A;Residues: 1-563 <STO>
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R; Takami, H.; Nakasone, K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match
14.3%; Score 402; DB 2;
Local Similarity; 26.7%; Pred. No. 3.1e-22;
hes 155; Conservative 82; Mismatches 260
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                                                                                                                                                                                                                                                                                                                                                                                                            IPEHVAIYEKLYQEYVTLHDYFGRGANDVMKRLKALKSIQH
                                                                                                                                                               GMLLGYTLQTKPEE----IYRALLEATAFGTRAIVDAFHGRGVEVHELYACGGLPQKNHLL
                                                                                                                                                                                                                                                                                                                                                                    VFGTSSCTMASTTSPSFVPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLDFHPAV---
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                                      --THVDKYYYPQERYQSLHH-----RRYEAYKQLQH
                                                                                                                      RQILADTCGIPVITTQCCEPVLLGSAILGAVAGNIA----PSVGEAMQQF---
                                                                                                                                                                                                       AVICGLGMERDLDNLLALYIAGLCGIGYGLRQILDAQTAQGVVSKNIVISGGAGQ-HPLV 452
                                                                                                                                                                                                                                             DEAQEKGVNVHALLE-----EKASQLRPGES-----GLLALDWWNGNRSILVDTELS
                                                                                                                                                                                                                                                                                   EEAREMAQRVNQPLPVWLADRILEKTAQ--PSDAVALAKGLHVVPEFLGNRAPFADPHAR 393
                                                                                                                                                                                                                                                                                                                              AMGTSICHMLLGEKEQEVEGMCGVVEDGIIPGYLGYEAGQSAVGDIFAWFVKHGVSAATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIVSPGTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAG----GIGTVGVEGGALNNLAY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFLEATDWIVSQMTGKIVKNSCTAGYKAIWHKREGYPSNEFFKALD-PRLEHLTTTKLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QFFDLADFLTWRATGDLARSVCTVTCKWTWLAHENRWDPDYFRTIGLAELADEDFIRIGH
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                                                                                MQIFADVTNREIKVAASKQTPALGAAMFASVAAGSEVGGYDSIEEAAKKMGRVKDETFKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji,
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R; Lee, N.; Carbon, J. PIDV. Acad. Sci. U.S.A. 74, 49-53, 1977

A;Title: Nucleotide sequence of the 5' end of arabab operon messenger RNA in Escherichia A;Reference number: I41134; MUID:77102763; PMID:189315

A;Accession: I41134
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C;Superfamily: ribulokinase
C;Keywords: arabinose metabolism; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizobu submitted to the EMBL Data Library, December 1992
A;Description: Systematic sequencing of the Escherichia coli genome: analysis of the 0-2 A;Reference number: $40531
A;Accession: $40579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-22,'S',24-126,'RS',129-349,'S',351-364,'A',366-402,'S',404-524,'R',526-566
A;Cross-references: GB:D10483; GB:J01597; GB:J01683; GB:J01706; GB:K01298; GB:K01990; GE
IDN:BAA01334.1; PID:g216483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 47, 231-244, 1986
A;TILLe: The organization of the araBAD operon of Escherichia coli.
A;Reference number: A91559; MUID:87163495; PMID:3549454
A;Accession: B29022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE000116; GB:U00096; NID:g1786240; PIDN:AAC73174.1; PID:g1786249, A;Experimental source: Strain K-12; Substrain MG1655 R;Lee, N.; Glelow, W.; Martin, R.; Hamilton, E.; Fowler, A. Gene 47, 231-244, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribulokinase (EC 2.7.1.16) - Escherichia coli (strain K-12) N;Alternate names: L-ribulokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: araB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:K01304; NID:g145312; PIDN:AAA23465.1; PID:g145313
C;Comment: This enzyme catalyzes the phosphorylation of L-ribulose to L-ribulose-5-phosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-14 < RES>
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A;Residues: 1-22,'S',24-126,'RS',129-349,'S',351-364,'A',366-402,'S',404-524,'R',526-566
A;Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA01334.1; PID:g216483
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Best Local :
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210 AELADEDFIRIGHHIVSP---
                                                         170 VAQSAASWIELCDWVPALLSGTTRPQDIRRGRCSAGHKSLW--HES-WG------GLPP 219
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                                                                                          ENPNAMFVLWKDHTAVEEAEEITRLCHAPGNVDYSRYIGGIYSSEWFWAKILHVTRQDSA 169
                                                                                                                                                                                                                                                                                                        FRHHPRDYIESMEAALKTVLAELSVEQRAAVVGIGVDSTGSTPAPIDADGNVLALRPEFA 109
                                                                                                                                                                                                                                           AKQN--IIVWMDHRATEQAERINATHHPVLN-----YVGGKISPEMETPKILWLKENMPE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                  IGLDFGSDSVRALAVDC-----ATGEEIATS-----VEWYPR--WQKGQFCDAPNNQ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGVDVGSGSVRAGIFDLNGSLLSHAT-EKITTTRRSGSRVEQSSQEIWQ--AVCSCIRNA 64
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nilarity 28.1%;
Conservative 7:
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75; Mismatches
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-GTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAG 261
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les 221;
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                                                                                                                                                                                                                                                                                                                                                                                 262 GIGTVGVEGGALNNLAYVFGTSSCTMASTTSPSF----VPGVWGPYYSAMVPGLWLVEGG 317
AAIFAAVAAKVHADIPSAQQKMASAVEKTLQPCSEQAQRFEQL-YRRYQQW
                                                                                 FGARAIMECFTDQGIAVNNVMALGGIARKNQVIMQACCDVLNRPLQIVASDQCC---ALG
                                                                                                                                                                     TEAWAKNPSLDHLPVVLDWFNGRRTPNANQRLKGVITDLNLATDAPLLFGGLIA---ATA 435
                                                                                                                                                                                                                                                        QSAFGDIYAWFGRVLGWPLEQLAAQHP-----ELKTQINAS--
                                                                                                                                                                                                                                                                                                QSA-----AGAAIDQLLDFHPAVEEAREMAQRVNQPLPVWLADRILEKTAQPSD 366
                                       SAILGAVAGNIAPSVGEAMQQF-THVDKYYYP----QERYQSLHHRRYEAY 522
                                                                                                                           YGLRQILDAQTAQGVVSKNIVISGG-AGQHPLVRQILADTCGIP---VITTQCCEPVLLG 476
                                                                                                                                                                                                                                                                                                                                                                                                                           ASFFDELDPILNRHLPSPLFTDTWTADIPVGT-LCPEWAQRLGLPESVVISGGAFDCHMG
                                                                                                                                                                                                                                                        ----QKQLLPAL 378
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Search completed: March 13, 2003, 16:56:01 Job time: 21.5662 secs

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Total number of hits satisfying chosen parameters: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. seq length: 0 seq length: 2000000000 protein search, using sw model % Query Match BLOSUM62 Gapop 10.0, US-09-802-208B-4 2811 March 13, 2003, 16:42:27; Search time 10.6093 Seconds (without alignments) 2087.642 Million cell updates/sec 112892 seqs, 41476328 residues 116.0 114.1 114.1 114.1 113.4 113.4 113.3 113.4 113.3 113.4 113.3 113.4 113.5 SwissProt_40:* MTITKTVIGVDVGSGSVRAG.....HHRRYEAYKQLQHTAKLLRD Copyright Length $\begin{array}{c} 5.55 \\ 5.$ GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd. DΒ Gapext 0. ARAB_MYCSM
ARAB_ECOLI
ARAB_SALTY
ARAB_YERPE
MP43_YEAST
ARAB_STANM
XYLB_LACPE
GLPK_MOUSE
YDEV_ECOLI
GLPK_PASMU
GLPK_PASMU
GLPK_ENTCA
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GCPK_ENTFA
GLPK_LACLA
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GLPK_BACSU
CTYKK_PASMU
XYLB_ECOLI
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45	44	43	42	41	40	39	38	37	36	35	34
261	263.5	267.5	270.5	270.5	271.5	271.5	271.5	276.5	278.5	279.5	282
9.3	9.4	9.5	9.6	9.6	9.7	9.7	9.7	9.8	9.9	9.9	10.0
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XYLB_LACLA	GLPK_RHIME	GLPK_MYCLE	GNTK_BACLI	GLPK_THEAQ	GLPK_CAEEL	GLPK_ECOLI	GLK2_THEMA	GLPK_PYRKO	GLPK_AQUAE	GLPK_BACHD	GLPK_PSETO
Q9cfg8 lactococcus	~	Q9cb81 mycobacteri		09wx53 thermus aqu	Q21944 caenorhabdi	P08859 escherichia	Q9x1e4 thermotoga	093623 pyrococcus		Q9kdw8 bacillus ha	

ALIGNMENTS

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edo V., Bertero M.G., Bessieres P., Bolotin A., Borcher iss R., Bourster L., Brans A., Braun M., Brignell S.C., Caldwell B., Capuano V., Carter S.K., Codani J.J., Connerton I.F., Cummings N.J., Danizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmer an K.D., Erington J., Fabret C., Ferrari E., Foulger E. C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galler S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G. S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G. S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G. S., Hullo M.F., Itaya M., Gepti G., Guy B.J., Haga K., Haiech J., Harwood C.R., Heert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., S. B., Karamata, D., Kasahara Y., Klaerr-Blanchard M., Klysahi Y., Koetter P., Koningstein G., Krögh S., Kumanota K., Lapidus A., Lardinois S., Lauber J., Lazarevic V. S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue B., Can N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Ne e D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Par O V., Pohl T.M., Portetelle D., Porwollik S., Prescott eran E., Polita C., Rocha E., Roche B., Rose M., Sadaie T., Scanlan E., Schleich S., Schroeter R., Scoffone F.	[2] SEQUENCE FROM N.A. STRAIN-168; MIDALINE-97124191; PubMed-8969504; MIDALINE-97124191; PubMed-8969504; MIDALINE-97124191; PubMed-8969504; MIDALINE-97124191; PubMed-8969504; MIDALINE-97124191; PubMed-8969504; MIDALINE-97124191; PubMed-8969504; MIDALINE-97124191; PubMed-9384377; MEDLINE-97124191; MIDALINE-97124191; ; MIDALINE-97124191; MIDALINE-97124191; MIDALINE-97124191; MIDALINE-97124191; MIDALINE-9712419191; MIDALINE-97124191; MIDALINE-97124191; MIDALINE-97124191; MIDALINE-97124191; MIDALINE-971241	Bacillus subtilis. Bacteria; Firmicutés; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1423; [1] SEQUENCE FROM N.A. STRAIN=168; STRAIN=168; MEDILINE=97237725; PubMed=9084180; Sa-Nogueira I.M.G., Nogueira T.V., Soares S., de Lencastre H.; "The Bacillus subtilis L-arabinose (ara) operon: nucleotide sequence, genetic organization and expression."; Microbiology 143:957-969(1997).	AAB_BACSU STANDARD; PRT; 560 AA. P94524; 005185; 01-NOV-1997 (Rel. 35, Created) 15-JUN-2002 (Rel. 41, Last annotation update) L-ribulokinase (EC 2.7.1.16).

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Best Local S
Matches 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconl E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Togonoi A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtills.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00370; FGGY; 1
Pfam; PF02782; FGGY_C; 1.
TIGRFAMS; TIGR01234; L-ribulokinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in Bacillus subtilis.";
mol. Microbiol. 33:476-489(1999).
-i- CATALYTIC ACTIVITY: ATP + L-ribulose = ADP + L-ribulose 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSCRIPTIONAL REGULATION. PubMed=10417639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Kinase; CONFLICT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mota L.J., Tavares P., Sa-Nogueira I.M.G.;
"Mode of action of AraR, the key regulator of L-arabinose metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
      298
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                                                                                                                                                                                                                                                                                                                                                                                                                 8 IGVDVGSGSVRAGIFDL-NGSLLSHATEKI-----TTTRRSGSRVE-----QSSQEIWQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphate.

PATHWAY: L-arabinose catabolism; second step.

INDUCTION: Transcription is repressed by glucose and by the binding of arak to the operon promoter. L-arabinose acts as inducer by inhibiting the binding of arak to the DNA, thus allowing expression of the gene.

SIMILARITY: BELONGS TO THE RIBULOKINASE FAMILY.
VLLGEEVHIVPGMCGVVDNGILPGYAGYEAGQSCVGDHFDWFVKTCVPPAYQEEAKEKNI
                                                                                                    GTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIGTVGV-EGGALNNLAYVFGTSSCT
                                        MASTTSPSFVPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLD--FHPAV-EEARE---
                                                                                                                                                                                              DFLTWRATGDLARSVCTVTCKWTWLAHENRWDPDYFRTIGLA-ELADEDFIRIGHHIVSP
                                                                                                                                                                                                                                                                         DHRATEQAERIN----ATHHPVLNYVGGKISPEMETPKILWLKENMPEIYERAGQFFDLA
                                                                                                                                                                                                                                                                                                                 VLETTIPSLLEQTGVDPKDIIGIGIDFTACTILPIDSSGQPLCMLPEYEEEPHSYVKLWK 124
                                                                                                                                                                                                                                                                                                                                       GEKAGS-LTEKMAKLTGLLPGTAVAVANVDAHV-SVPAVGITEPG---KMLMIMGTSTCH
                                                                                                                                                        DWIVYQLCGSLKRSNCTAGYKAMWSEKAGYPSDDFFEKLNPSMKTITKD--KLSGSIHSV
                                                                                                                                                                                                                                    HHAAQKHADRLNQIAEEEGEAFLQRYGGKISSEWMIPKVMQIAEEAPHIYEAADRIIEAA
                                                                                                                                                                                                                                                                                                                                                                                           IGVDFGTLSGRAVLVHVQTGEELAAAVKEYRHAVIDTVLPKTGQKLPRDWALQHPADYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    560 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.0%; Score 448.5; DB 1; Length 560; 27.1%; Pred. No. 4.4e-25;
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-i- CATALYTIC ACTIVITY: ATP + L-ribulose = ADP + L-ribulose 5-
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MEDLINE-21074935; PubMed-11206551;

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                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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SEQUENCE FROM N.A. STRAIN=C-125 / JCM MEDLINE=20512582;

JCM 9153;

PubMed=11058132;

Bacillus halodurans. Bacteria; Firmicutes;

Bacillales;

Bacillaceae;

Bacillus

ARAB OR BH1872 15-JUN-2002 15-JUN-2002 L-ribulokinase (EC

NCBI_TaxID=86665;

Q9KBQ3; 15-JUN-2002

(Rel. 41, Created)
(Rel. 41, Last sequence up
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ase (EC 2.7.1.16).

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SEQUENCE 565 AA; 61096 MW; 45E7D9AA096B9CAD CRC64;
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ilarity 27.78;
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Pred. No. 5.8e
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InterPro; IPR000577; FGGY_kin.
Pfam; PF00370; FGGY; 1.
Pfam; PF02782; FGGY_C; 1.
TIGREPAMS; TIGR01234; L-ribulokinase; 1.
Transferase; Kinase; Arabinose catabolism; Complete proteome.
SEQUENCE 563 AA; 61668 MW; CCBC399006669ACD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-I- CATALYTIC ACTIVITY: ATP + L-ribulose = ADP + L-ribulose
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Fuji F., Hirama
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IPEHVAIYEKLYQEYVTLHDYFGRGANDVMKRLKALKSIQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -IIVWMDHRATEQAERIN----ATHHPVLNYVGGKISPEMETPKILWLKENMPEIYERAG
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                                 --THVDKYYYPQERYQSLHH-----RRYEAYKQLQH
                                                                    MQIFADVTNREIKVAASKQTPALGAAMFASVAAGSEVGGYDSIEEAAKKMGRVKDETFKP
                                                                                                       RQILADTCGIPVITTQCCEPVLLGSAILGAVAGNIA----PSVGEAMQQF------
                                                                                                                                        GMLLGYTLQTKPEE----IYRALLEATAFGTRAIVDAFHGRGVEVHELYACGGLPQKNHLL
                                                                                                                                                                           AVICGLGMERDLDNLLALYIAGLCGIGYGLRQILDAQTAQGVVSKNIVISGGAGQ-HPLV
                                                                                                                                                                                                                  DEAQEKGVNVHALLE---
                                                                                                                                                                                                                                                 EEAREMAQRVNQPLPVWLADRILEKTAQ---PSDAVALAKGLHVVPEFLGNRAPFADPHAR
                                                                                                                                                                                                                                                                                    AMGTSICHMLLGEKEQEVEGMCGVVEDGIIPGYLGYEAGQSAVGDIFAWFVKHGVSAATF
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irama C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.3%; Score 402; DB 1; Length 563; 26.7%; Pred. No. 1e-21; Live 82; Mismatches 260; Indels
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Best Local
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InterPro; IPR00577; FGGY_kin.
Pfam; PF00370; FGGY_C; 1.
Pfam; PF02782; FGGY_C; 1.
TIGRPAMS; TIGR01234; L-ribulokinase; 1
Transferase; Kinase; Arabinose catabol.
SEQUENCE 563 AA; 60432 MW; 12F09759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soda A., Takata G., Izumori K.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ d
-!- CATALYTIC ACTIVITY: ATP + L-ribulose - ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002
15-JUN-2002
15-JUN-2002
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Bacteria; Actinobacteria;
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PATHWAY: L-arabinose catabolism;
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                              DPHARAVICGLGMERDLDNLLALYIAGLCGIGYGLRQILDAQTAQGVVSKNIVISGGAGQ
                                                                                                                                                                                               ----EDFIR--IGHHIVSPGTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIGTVGV
DHHLSGIMVGQTLD---TTCVDQYRALLEATAFGTRMIVETFQRSGVPVEELVVAGGLIK
                                                          TKNCVPKETATEASRR----
                                                                                     LDFHPAVEEAREMAQRVNQPLPVWLADRILEKTAQPSDAVALAKGLHVVPEFLGNRAPFA
                                                                                                                        DPG---RLIAIMGTSTCHVMNGRFLREVPGMCGVVDGGITDGLWGYEAGQSGVGDIFAWF
                                                                                                                                                                                                                                                                           IYERAGQFFDLADFLTWRATGDLARSVCTVTCKWTWLAHENRWDPDYFRTIGLAELAD --
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                                                                                                                                                    EGGALNNLAYVFGTSSCTMASTTSPSFVPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQL
                                                                                                                                                                                  ASFVEDKIEQPIGRLGEAAGT ----LTAQAAAWTGLPEGIVVAVGNIDAHVTAAAADAA
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2 (Rel. 41,
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EC 2.7.1.16).
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annotation
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Pred. No. 2.4e-21
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  catabolism.
  12F097597D07918C CRC64;
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P08204; P78041;

01-AUG-1988 (Rel. 08, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                              J. Biol.
    use by modified
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Yura T., Mori H., Nagai H., Nagata T.,
Isono K., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Escherich
the 0-2.4 min region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-87163495; PubMed-3549454;
Lee N., Gielow W., Martin R., Ham
"The organization of the arabad of Gene 47:231-244(1986).
                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARAB_ECOLI
                                                                                                                                                                                                                                                       "Nucleotide sequence of the L-arabinose Escherichia coli K12.";
                                                                                                                                                                                                                                                                                                    MEDLINE=79005683; PubMed=357433; Smith B.R., Schleif R.;
                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12;
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Proc. Natl. Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado Vides J., Glasner J.D., Rode C.K., Mayhew
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MEDLINE=97426617; PubMed=9278503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee N., Carbon J.;
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                                                                                                                                                                                                         siol. Chem. 253:6931-6933(1978).
CATALYTIC ACTIVITY: ATP + L-ribulose =
                                                                                                                                      PATHWAY: L-arabinose catabolism; second step. SIMILARITY: BELONGS TO THE RIBULOKINASE FAMILY.
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K., Mayhew G.F.,
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Pfam; PF00370; FGGY; 1.
Pfam; PF02782; FGGY_C; 1.
TIGRPAMs; TIGR01234; L-ribulokinase; 1.
TIGRPAMs; Tigr01234; L-ribulokinase; 1.
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EMBL; J01641; AAA23467.1; -.
EMBL; AE000116; AAAC73174.1; -.
EMBL; K01304; AAA23465.1; -.
EMBL; D10483; BAA01334.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECO2DBASE; D055.0; 6TH EDITION EcoGene; EG10053; araB. InterPro; IPR000577; FGGY_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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S40579; S40579,
                                                                                                                                                                            AVGA---
                                                                                                                                                                                              GIGTVGVEGGALNNLAYVFGTSSCTMASTTSPSF----VPGVWGPYYSAMVPGLWLVEGG
                                                                                                                                                                                                                                                                            ENPNAMFVLWKDHT,AVEEAEEITRLCHAPGNVDYSRYIGGIYSSEWFWAKILHVTRQDSA
                                                                                                                                                                                                                                                                                                                                  AKQN--IIVWMDHRATEQAERINATHHPVLN----YVGGKISPEMETPKILWLKENMPE
AAIFAAVAAKVHADIPSAQQKMASAVEKTLQPCSEQAQRFEQL-YRRYQQW
                    SAILGAVAGNIAPSVGEAMQQF-THVDKYYYP---
                                                         YGLRQILDAQTAQGVVSKNIVISGG-AGQHPLVRQILADTCGIP---VITTQCCEPVLLG
                                                                                    TEAWAKNPSLDHLPVVLDWFNGRRTPNANQRLKGVITDLNLATDAPLLFGGLIA---ATA
                                                                                                         AVALAKG-----LHVVPE-FLGNRAPFADPHARAVICGLGMERDLDNLLALYIAGLCGIG
                                                                                                                                QSAFGDIYAWFGRVLGWPLEQLAAQHP-----
                                                                                                                                                      QSA----
                                                                                                                                                                                                                                          AELADEDFIRIGHHIVSP-----GTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAG
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                                          FGARAIMECFTDQGIAVNNVMALGGIARKNQVIMQACCDVLNRPLQIVASDQCC---
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L-ribblokinase (EC 2.7.1.16).
ARAB OR STY0120.
Salmonol':
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P58542;
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15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterica serovar Typhi C
Nature 413:848-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead C. Barroll B.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CT18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGR01234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of a multiple enterica seroyar Typhi CT18.";
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PATHWAY: I
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VKVIGTSTCDILIADKQSVGDRAVKGICGQVDGSVVPNFIGLEAGQSAFGDIYAWFSRVL
                                                                                                                                                                                                                                                               IRNALT-LADVCAQSVAGIGFDATCSL-VVLDKNGDPLPVSPEGDAKQN--IIVWMDHRA
                                                                                                                                                                                                                                                                                                                             IGVDVGSGSVRAGIFD-LNGSLLSHATEKITTTRRS-----GSRVEQSSQEIWQAVCSC
                                                          RYPLFSETFTADLPVGT-LCAEWAQRLGLPESVVISGGAFDCHMGAVGA---
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                            AYVFGTSSCTMASTTSPSF----VPGVWGPYYSAMVPGLWLVEGGQSAAGA----
                                                                                                                        PALLSGTTRPQDIRRGRCSAGHKTLW--HES-WG-----
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                                                                                                                                                   -DLARSVCTVTCKWTWLAHENRWDPDYFRTIGL--AELADEDFIRIGHHI
                                                                                     GTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIGTVGVEGGALNNL
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0 BY SIMILARITY.
61643 MW; A1515DB7249A0F75 CRC6
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26.4%;
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Pred. No. 6.
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or send an email to license@fisb-sib.ch).
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Lin H.-C., Lei S.-P., Wilcox G.;
"The araBAD operon of Salmonella typhimurium LT2.
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15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
L-ribulokinase (EC 2.7.1.16).
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                                Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Creltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague."
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MEDLINE=21470413; PubMed=11586360;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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413:523-527(2001).
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SEQUENCE 563 AA; 61833 MW; 88EFIE0B00A5
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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-!- PATHWAY: L-arabinose catabolism; second step.
-!- SIMILARITY: BELONGS TO THE RIBULOKINASE FAMILY.
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MPA43 protein. MPA43 OR YNL249C OR N0875

update)

Saccharomyces cerevisiae (Baker's yeast).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-9288c / FYID/>;
MEDLINE-97377992; PubMed-9234673;
Medline-97377992; PubMed-9234673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X96722; CAA65495.1;
EMBL; Z71525; CAA96156.1;
EMBL; X94214; CAA63905.1;
SGD; S0005193; MPA43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 41-542 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis of the 33 kb from the left arm of chromosome Yeast 13:849-860(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-4932;
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                                                                                                                                                                                                              SSCTMASTT-SPSFVPGVWGPY------YSAMVPGLWLVEGGQSAAGAAIDQLL
                                                                                                                                                                                                                                                                                                                                                                                  WINMQCPQQLIDYLGGKFVPEMGVPKLKYFLDEYSHLRDKHFHIFDLHQYIAY----ELS
                                                                                                                                                         DFHPAVEEAREMAQRVNQPLPVWLADRILEKTAQPSDAVALAKGLHVVPEFLGNRAPFAD
                                                                                                                                                                                                                                                                                     VSPGTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAG--GIGTVGVEGGALNNLAYVFGT
                                                                                                                                                                                                                                                                                                                       R-----LYEWNIEGLLGRENLNGIGNDGEVSGWSSSFYKNI-----INLPSN-
                                                                                                                                                                                                                                                                                                                                                   RSVCTVTCKWTW-----LAHEN-------RWDPDYFRTIGLAELADEDFIRIGHHI
                                                                                                                                                                                                                                                                                                                                                                                                          RIN-ATHHPVLNYVGGKISPEMETPKILWLKENMPEIYERAGQFFDLADFLTWRATGDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTLADVCAQSVAGIGFDATCSLVVL--DKNGDPLPVSPEGDAKQNIIVWMDHRATEQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGVDVGSGSVRAGIFD-LNGSLLSHATEKITTTRRSGS---RVEQSSQEIWQAVCSCIRN 63
KNERLLSLIS
                             QHPLVRQILA 457
                                                           PRIKGSFIGESTDTSMLNLTYKYICILEFLSFQTKLIIDTFQNENSNIHIKELRISGSQA
                                                                                           PHARAVICGLGMERDLDNLLALYIAGLCGIGYGLRQILDA--QTAQGVVSKNIVISGGAG
                                                                                                                                                                                          SSCYMYGTTISDTRIPGVWGPFDTILDNRGDFSVYAA------GQSCTGKLIEHLF
                                                                                                                                                                                                                                                         VSIGT---TSLVANKHI-----STTVVRSCIDSYASWFAVASPHLE----TSLFMIAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LNIREYEVKSCGVSATCSLAIFERDRTSNMLIPYPNED----NVIFWMDSSAVNECQ
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443
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61667
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25.9%; Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKSWKFWQ -> RSHGNLA (IN REF. 830AA8D4E95365AD CRC64;
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XIV f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g region between ORC5 and SUI1
from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _STAAM
                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00370; FGGY; 1
Pfam; PF02782; FGGY_C;
Transferase; Kinase; A:
SEQUENCE 545 AA; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP003359; BAB56714.1; -. EMBL; AP003130; BAB41741.1; -. InterPro; IPR000577; FGGY_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus (strain Mu50
Staphylococcus aureus (strain N315)
Bacteria; Firmicutes; Bacillales; S
NCBI_TaxID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
L-ribulokinase (EC 2.7.1.16).
ARAB OR SAV0552 OR SA0510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lancet 357:1225-1240(2001).
-!- CATALYTIC ACTIVITY: ATP + L-ribulose - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Mu50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole genome sequencing of meticillin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21311952;
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                                                                                                                                                                                                                                                                                                                                                                Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphate.
PATHWAY: [
                                IVSPGTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIGTVGVEGGALNNLAYVFGTS
                                                                                               DLADFLTWRATGDLARSVCTVTCKWTWLAHENRWDPDYFRTIG--LAELADEDFIRIGHH
                                                                                                                                                                                                                                                                                             IGVDVGSGSVRAGIFD-LNGSLLSH----ATEKITTTRRSGSRVE-----QSSQEIWQAV
 VVNIGEVVGK-LDDKMAQKLGLSKETMVSPFIIDAHASLLG-IGSEKD--KEMTMVMGTS
                                                                                                                                                               VWMDHRATEQAERINAT----HHPVLNYVGGKISPEMETPKILWLKENMPEIYERAGQFF
                                                                                                                                                                                               EEGISYIVRESKIDPVNIVGIGIDFTSSTIIFTDEN-----LNPVHNLKQFKNNPHAYVK
                                                                                                                                                                                                                                CSCIRNALTLADVCAQSVAGIGEDATCSLVVL-DKNGDPLPVSPEGDAKQ-----NII 109
                                                                                                                                                                                                                                                                IGIDYGTASGRVFLINTINGQVVSKFVKPYTHGVIESELNGLKIPHTYALQNSNDYLEIM
                                                                EAGDWIVNKLTNKNVRSNCGLGFKAFW-EEETGFHYDLFDKIDPKLSKVIQD----KVSAP
                                                                                                                               LWKHHGAYKEAEKLYQTAIENNNKWLGHYGYNVSSEWMIPKIMEVMNRAPEIMEKTAYIM
                                                                                                                                                                                                                                                                                                                                140;
                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=11418146;
                                                                                                                                                                                                                                                                                                                                                                                                 60965
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGGY_kin.
                                                                                                                                                                                                                                                                                                                                                12.18; 24.78;
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                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                               109;
                                                                                                                                                                                                                                                                                                                                              Score 340; DB 1;
Pred. No. 3.1e-17;
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                                                                                                                                                                                                                                                                                                                                                                                               catabolism; Complete pr
E3917036237CEA4B CRC64;
                                                                                                                                                                                                                                                                                                                               Mismatches 245;
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                                                                                                                                                                                                                                                                                                                                72;
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RESULT 12

XYLB_LACPE
ID XYLB_LACPE
ID 01-MAY
DT 01-FEB
DE XYLB.
OS Lactob
OC Lactob
OX STRAIN
RX LORMAN
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CC -!- SI
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01-FEB-1995 (Rel. 31, Last annotation update)
Xylulose kinase (EC 2.7.1.17) (Xylulokinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Posno M., Pouwels P.H.;
"Organization and characterization of three genes
"Oryalose catabolism in Lactobacillus pentosus.";
Mol. Gen. Genet. 230:161-169(1991).
                                                                                                                                                                                                                      PROSITE; PS00445; FGGY_KINASES_2; 1.
PROSITE; PS00933; FGGY_KINASES_1; 1.
                                                                                                                                                                                                                                                                       Pfam; PF02782; FGGY_C; 1.
TIGRFAMs; TIGR01312; XylB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92079891; PubMed-1660563;
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                                                                                                                                                                                                    Transferase;
                                                                                                                                                                                                                                                                                                                          Pfam; PF00370; FGGY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000577; FGGY_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lokman B.C., van Santen P., Verdoes J.C., Kruese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactobacillus pentosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphate.
SIMILARITY: BELONGS TO THE FUCOKINASE / GLUCONOKINASE
GLYCEROKINASE / XYLULOKINASE FAMILY.
S18562; S18562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L----FKAYKALHDIHGYKKANIMKD
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23.7%;
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                                                                                                                                                                           ME:
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                                                                       Score 325; DB Pred. No. 3.4e 0; Mismatches
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                                                                       DB 1; I
3.4e-16;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glycerol kinase (EC, 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
(Glycerokinase) (GK).
                                          "Isolation, mapping, and functional chromosome glycerol kinase gene."; Genomics 36:530-534(1996).
                                                                                                                                                                                                       MEDLINE-97038697; PubMed=8884278;
Hug A.H., Lovell R.S., Sampson M.
Disteche C.M., Craigen W.J.;
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                               GLPK_MOUSE
Q64516;
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                FUNCTION: KEY ENZYME IN THE REGULATION OF
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                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;

    STIGANGLLFAPYIVGERAPYADATIRGSFIGVDGS

                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                       M.J.,
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Best L
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HSSP; P08859; 1GLJ.

MGD; MGI:106594; Gyk.

InterPro; IPR000577; FGGY_kin.

Pfam; PF00370; FGGY; 1.

Pfam; PF02782; FGGY_C; 1.

TIGRFAMS; TIGR01311; glycerol_kin; 1.

PFAMSITE; PS00345; FGGY_KINASES_1; 1.

PROSITE; PS00333; FGGY_KINASES_1; 1.

RPGGIFE; PS00333; FGGY_KINASES_1; 1.

Glycerol metabolism; Transferase; Kinase; ATP-binding.

MGlycerol metabolism; Transferase; Kinase; ATP-binding.

NP_BIND 167 179 ATP (PR0BABE).
                                                 01-NOV-1997 (Rel. 35, Create 01-NOV-1997 (Rel. 35, Last st 16-OCT-2001 (Rel. 40, Last an Hypothetical sugar kinase yde YDEV OR B1511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                  V_ECOLI
YDEV_ECOLI
P77432; Q998
01-NOV-1997
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                            Escherichia coli.
Bacteria; Proteobacteria;
   NCBI_TaxID=562;
                  Escherichia
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                                                                                                                                                                                                                       SNKILMQLQADILYIPVVKPSMPETTALGAAMAAGAAEGV
                                                                                                                                                                                                                                                OHPLVROILADTCGIPVITTQCCEPVLLGSAILGAVAGNI
                                                                                                                                                                                                                                                                                                  DPHARAVICGLGMERDLDNLLALYIAGLCGIGYGLRQILDAQTAQ-GVVSKNIVISGGAG
                                                                                                                                                                                                                                                                                                                                                                                              GTGCFLLCNTGHKCVFSEHGLLTTVAYKLGRDKPVYYAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLADFLTWRATGDLARSV-CT--VTCKWTWL--AHENRWDPDYFRTIGLAELADEDFIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAVLGPLVGAVDQGTSSTRFLVFNSKTAELLSHHQVEIKQEFPREGWVEQDPKEILQSVY
                                                                                                                                                                                                                                                                                EPSARGIICGL-
                                                                                                                                                                                                                                                                                                                                        RDNLGIIKSSEE
                                                                                                                                                                                                                                                                                                                                                                LDFHPAVEEAREMAQRVNQPLPVWLADRILEKTAQPSDAVALAKGLHVVPEFLGNRAPFA
                                                                                                                                                                                                                                                                                                                                                                                                                      GTSSCTMAST-----TSPSFVPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPNVRSSSEIYG-----LMKAGALEGVPISGCLGDQSAALVGQMCFQDGQAKN---TY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHHIVSPGTPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIGTVGVEGGALNNLAYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIDSWLIWSLTGGIHGGVHCTDVTNASRTMLFNIHSLEWDKELCEFFGIP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRTQSTVENLSKRIPGNNNFVKSKTGLPLSTYFSAVKLRWLLDNVKKVQEAVEENRALFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRATEQAE----RINATHHPVLNYVGGKISPEMETPKILWLKENMPEIYERAGQ----FF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECIEKTCEKLGQLNIDISNIKAIGVSNQRETTVVWDKVTGEPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCIRNA---LTLADVCAQSVAGIGF-DATCSLVVLDK-NGDPLPVSPEGDAKQNIIVWMD
                                                                                                                                   Q99894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                STANDARD;
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25.6%; Pred. No. 4.6e-16;
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                            gamma
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                              subdivision;
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                            Enterobacteriaceae;
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Best Local S
Matches 142
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REMBL; D90794; BAA15191.1; ...

REMBL; D90794; BAA15198.1; ...

REMBL; S82185; AAC17184.1; ...

RECOGENE; EG13804; ydev. ...

RINTERPROJECT, FGGY_KIN.

RINTERPROJECT, FGGY_C; 1...

RP FAMM; PF00370; FGGY_C; 1...

RP PF03770; FGGY_KINASES_1; FALSE_NEG.

RPROSITE; PS00933; FGGY_KINASES_1; FALSE_NEG.

RPROSITE; PS00945; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00445; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00445; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00445; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00445; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS0045;  FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITE; PS00465; FGGY_KINASES_2; FALSE_NEG.

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RPROSITES PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITES PS00465; FGGY_KINASES_2; FALSE_NEG.

RPROSITES PS00465; FGGY_K
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Oncogene 12:947-951(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 182-495 FROM N.A.
MEDLINE=96243037; PubMed=8649811;
Das R., Reddy E.P., Chatterjee D.,
"Identification of a novel Bcl-2 r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence Science 277:1453-1474(1997).
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MEDLINE=97426617; Pu
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                                     64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCEROKINASE / XYLULOKINASE FAMILY.

CAUTION: WAS THOUGHT BY REF. 3 TO BE A HUMAN SEQUENCE AND WAS CALLED BY THEM BRAG1 (BRAG1-1)

WITH A ROLE IN APOPTOSIS. THE DNA SEQUENCE OF THE REGION THEI SEQUENCED IS MORE THAN 99% IDENTICAL TO THAT OF THIS E. COLI SEQUENCED IS MORE THAN 99% IDENTICAL TO THAT OF THIS E. COLI GENE. FURTHERMORE THEY CLAIM 'EXTENSIVE SIMILARITY TO THE BCL-2 FAMILY OF GENES.' SUCH A SIMILARITY IS NOT SIGNIFICANT AND THIS PROTEIN IS MUCH MORE LIKELY TO BE A SUGAR KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE FUCOKINASE
ALTLADVCAQSVAGIGFDATCS---
                                                                                                                                                       VIGVDVGSGSVRAGIFDLNGSLLSHATEK---ITTTRRSGSRVEQSSQEIWQAVCSCIRN
                                                                                                             LMALDAGTGSTRAVIFDLEGNQIAVGQAEWRHLAVPDVPGS-MEFDLNKNWQLACECMRQ
                                                                                                                                                                                                                                                             142;
                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9278503;
                                                                                                                                                                                                                                                                                            11.5%;
                                                                                                                                                                                                                                                      74;
                                                                                                                                                                                                                                                      Score 323; DB
Pred. No. 5.1e
74; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Escherichia coli K-12.";
-LVVLDKNGDPLPVSPEGDAKQNIIVW----MDHR:|: | : | | : | |
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related gene,
                                                                                                                                                                                                                                                                                            DB 1;
.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLUCONOKINASE
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                                                                                                                                                                                                                                                                                                                                 Length
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H., Mori T.,
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                                                                                                                                                                                                                                                         152;
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                                                                                                                                                                                                                                                         Gaps
                                                                                                                 72
                                                                                                                                                                                     63
                                                                                                                                                                                                                                                         26;
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RESULT 15

XYLB_BACSU
ID XYLB_B
AC P39211
DT 01-FEB
DT 01-FEB
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A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Liardinois S., Lauber J., Lazarevic V.,
Mannica W. Tarica N. Hill Mannida G. Mannil C. Machine C.,
Mannica W. Tarica N. H., Lardinois S., Lauber J., Lazarevic V.,
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01-NOV-1997
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P39211;
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
nase (EC 2.7.1.17) (Xylulokinase).
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                          Liu H., Masuda
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PROSITE; PS00933; FGGY_KINASES_1; 1.
Transferase; Kinase; Xylose metabolism; Complete
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Wilhelm M., Hollenberg C.P.;
"Nucleotide sequence of the Bacillus subtilis xylose isomerase
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93; Mismatches
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Q8u7x5 agrobacteri
Q8ybc1 brucella me
Q8zaz2 yersinia pe
Q9m0c9 arabidopsis
Q98d08 rhizobium n
Q9vzj8 drosophila
Q9vzj8 drosophila
Q9u7j6 agrobacteri
Q9Gc1 homo sapien
Q9fc2 neurospora
Q04585 saccharomyc
Q95t84 drosophila
Q9ha63 homo sapien
Q92ui5 rhizobium m
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ALIGNMENTS

Db 1 Db 61	Query Ma Best Loc Matches	KW Kinase. SQ SEQUENCE	DR Pfam; DR Pfam; DR TIGRF			OX NCBI_TaxI RN [1] RP SEQUENCE RC STRAIN=C;			RESULT 1 Q9F4L6 ID Q9F4L6
	Query Match 100.0%; Score 2811; DB 2; Length 534; Best Local Similarity 100.0%; Pred. No. 2.7e-187; Matches 534; Conservative 0; Mismatches 0; Indels 0; G	e. NCE 534 AA;	<pre>Pfam; PF00370; FGGY; 1. Pfam; PF02782; FGGY_C; 1. TIGRFAMS; TIGR01315; 5C_CHO_kinase; 1.</pre>	Submitted (JUL-2000) to the EMBL/GenBank/DDBJ EMBL; AY005817; AAG01884.1; - InterPro; IPR000577; FGGY_kin.	<pre>LaFayette P.R., Pairott W.A.; "A non-antibiotic marker for amplification of vectors in E. coli";</pre>	NCBI_TaxID=562; [1] SEQUENCE FROM N.A., STRAIN=C;	RTLK. RTLK. Escherichia coli. Bactheria; Proteobacteria; gamma subdivision; Escherichia.	01-MAR-2001 (TrEMBLrel. 01-MAR-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. Ribitol kinase	6 PRELIMINARY;
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LSHATEKITTTRRS LDKNGDPLPVSPEG	Score 2811; DB 2; Pred. No. 2.7e-187; Mismatches 0;	F62DD4B966556875	e; 1.	GenBank/DDBJ d			ubdivision; En	Created) Last sequence update) Last annotation update)	; 534 AA.
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                                                             Kinase.
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STRAIN-1033-5p14;

MEDITINE-97464425; PubMed-9324246;

Heuel H., Turgut S., Schmid K., Lengeler J.

"Substrate recognition domains as revealed the D-arabinitol and ribitol transporters f pneumoniae.";

"Bacteriol. 179:6014-6019(1997).
                                                                             Microbiology 144:1631-1639(1998).
EMBL; AF045244; AAC26495.1; -.
InterPro; IPR000577; FGGY_kin.
Pfam; PF00370; FGGY; 1.
Pfam; PF02782; FGGY_C; 1.
TIGRFAMS; TIGR01315; 5C_CHO_kinase;
                                                                                                                                          "Genes for D-arabinitol and pneumoniae.";
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Heuel H., Shakeri-Garakani A., Tu
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Goodner B., Qurollo B., Houmiel K., Wollam C., A
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Okura V.K., Zhou Y., Chen L., Wood G.E., Alneida N.F. Jr.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.
                                                          SEQUENCE FROM N.A. MEDLINE=21608551;
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01-JUN-2002
                                                                                                 Science
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NCBI_TaxID=176299;
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E=21608551; PubMed=11743194;
IE=21608551; PubMed=11743194;
Ir B., Hinkle G., Gattung S., Miller N., Blanchard M.,
O B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mull
I K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
I C., Allinger M., Doughty D., Scott C., Lappas C., Markel
an C., Crowell C., Gürson J., Lomo C., Sear C., Strub G.,
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Agrobacterium tumefaciens C58. Science 294:2323-2328(2001). EMBL; AE009360; AAL45118.1; -. EMBL; AE008352; AAK89115.1; -.

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STRAIN-16M / ATCC 23456 / BIOTYPE 1;

MEDLINE-20020109; PubMed-11756688;

Delvecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Rez Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson Haselkorn R., Kyrpides N., Overbeek R.,
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SEQUENCE
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01-MAR-2002 (TrEMBLrel. 20, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
D-ribulokinase (EC 2.7.1.47).
                                                                                                         Bacteria; Proteobacteria;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                          Brucella melitensis
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EMBL; AE009731; AAL54221.1; -
InterPro; IPR000577; FGGY_kin.
Pfam; PF00370; FGGY; 1.
Pfam; PF02782; FGGY_C; 1.
TIGRFAMS; TIGR01315; 5C_CHO_kinase;
STRAIN-CO-92 / BIOVAR ORIENTALIS;
MEDLINE-21470413; PubMed-11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.
Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga.
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Chillingworth T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Putative carbohydrate kinase.
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                                                                                                                                                                                                                                                 Yersinia.
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Pred. No. 2.4e:
56; Mismatches
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e-100;
155; Indels
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Best Local Sim
Matches 241;
                                                                            O9MOC9
PRELIMINARY; PRT; 569 AA.

Q9MOC9;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2000 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 61.5 kDa protein.
AT4630310.
AT4630310.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
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Pfam; PF02782; FGGY_C; 1.

TIGRAMS; TIGR01315; CCHO_kinase; 1.

PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

Kinase; Hypothetical protein; Complete proteome.

SEQUENCE 545 AA; 59461 MW; 7E50F6B7F24D93A2
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Simmonds M.,
Lamar B., Stoneking
Mayer K.F.X.;
                                             SEQUENCE FROM
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rocal Similarity
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                                               N.A.
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J., Stevens
                        Stumpf
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100; Mismatches
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evens K.,
n pestis,
                      J.,
                           Mewes
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Best Loc
Matches
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ da
EMBL; AL161576; CAB81024.1; -.
InterPro; IPR000577; FGGY_kin.
Pfam; PF00370; FGGY; 1.
Pfam; PF00370; FGGY; 1.
Pfam; PF02782; FGGY_C; 1.
TIGRFAMS; TIGR01315; 5C_CHO_kinase; 1.
Hypothetical protein.
SEQUENCE 569 AA; 61462 MW; 894A659FDF4CB0C6
                                                           Q98D08 PRELIMINARY;
Q98D08 PRELIMINARY;
01-OCT-2001 (TrEMBLrel. 1
01-OCT-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
Ribitol kinase.
                            Rhizobium loti (Mesorhizobium lo
Bacteria; Proteobacteria; alpha
Phyllobacteriaceae; Mesorhizobiu
                Phyllobacteriaceae;
NCBI_TaxID=381;
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SEQUENCE
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          Q92N09;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence upda)
Q1-DEC-2001 (TrEMBLrel. 21, Last annotation up Putative sugar kinase protein (EC 2.7.1.).
R02438 OR SMC01503.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
NCBL_TaxID-382;
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KENUENCE 528 AA;
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EMBL; AP003005; BAB51463.1; -.
Interpro; IPR000577; FGGY_kin.
Pfam; PF00370; FGGY; 1.
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"Complete genome structure of the nitrogen-fixing symbiotic bac
                                                                                                                                                            Q92N09
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TIGRFAMs; TIGR01315; 5C_CHO_kinase;
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Pred. No. 1.3e-65;
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Mismatches 178;
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Best Local S
Matches 223
O9VZJ8 PRELIMINARY;
O9VZJ8;
O1-MAY-2000 (TrENBLrel. 1:
O1-MAY-2000 (TrENBLrel. 1:
O1-JUN-2002 (TrENBLrel. 2:
CG11594 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Botstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium melilicti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

EMBL; AL591790; CAC47017.1; -. InterPro; IPR000577; EGGY_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00370; FGGY; 1.
Pfam; PF02782; FGGY_C; 1.
TIGRFAMS; TIGR01315; SC_CHO_kinase;
Transferase; Complete proteome.
SEQUENCE 527 AA; 57700 MW; 9F37/
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                                                                                                                                                                                                                                         461
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                                                                                                                                                                          521 EEL 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 VIGVDVGSGSVRAGIFDLNGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNALT
                                                                                                                                                                                                                                                                                                                                                                                                                                 F--GMWGPYFEAVLPGLWLIEGGQSATGALLDHIVRLHGGGLPPTTETHAKIIERVQEMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHPVLNYVGGKISPEMETPKILWLKENMPEIYERAGOFFDLADFLTWRATGDLARSVCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAVDIGTGSARAGVEDRRGKLLARADRTIAMNRPEENHAEHDSEDIWAAVCGAVRSARE
                                                                                                                                                                                                                                                                                                                                                                                   AEMGLLPGTPVAVGLIDAHAGGIGTVGVEGGA----LNNLAYVFGTSSCTMA--STTSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAAVPAESIAAIGFDATCSLVVRDRDGAPLSVNRQGEARWDTIVWLDHRALAEADFCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LADVCAQSVAGIGFDATCSLVVLDKNGDPLPVSPEGDAKQNIIVWMDHRATEQAERINAT
                                                                                                                                                                                                        AKL 531
                                                                                                                                                                                                                                       PDAVLLGTAMTAAVAGELYPDLASAGPAMSSAGTERLPDPALRRIYDRDYRRFLALYRHR
                                                                                                                                                                                                                                                                       CEPVLLGSAILGAVAGNIAPSVGEAMQQFTHVDKYYYPQERYQSLHHRRYEAYKQL-QHT
                                                                                                                                                                                                                                                                                                      RLYWRTCVAIALGIRHILEMMKEAGYELDTLHVTGGHVRNPLLMELYCDVTGCRVVAPQA
                                                                                                                                                                                                                                                                                                                                  ALYIAGLCGIGYGLRQILDAQTAQGVVSKNIVISGGAGQHPLVRQILADTCGIPVITTQC
                                                                                                                                                                                                                                                                                                                                                                    AVHGAD-----FAQRLHVLPDFHGNRSPLADPHALGVISGLPLDSSFDALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLDFH-----PAVEEAREMAQRVNQPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EELGLDTGCQVAPGLIDAYAGALGVLGGFADAPAKLERQLALIGGTSSCIVAFSKDMKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAKWNYLAHERRGWQQDYLEQIGLEDLLERGGLPEETLPVERAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCKWTWLAHENR-WDPDYFRTIGLAELAD-----EDFIRIGHHIVSPGTPCGNGLTAQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHPVLDHSGRVMSPEMEMPKLMWLKRNLPQQWERAGYFFDLADYMSWRSTGSTARSRCTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.4%; Score 1050; DB 16
41.1%; Pred. No. 7.4e-65;
ative 90; Mismatches 188
                             Created)
Last sequence update)
Last annotation update)
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                                                                                               548
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                                                                                                                                                                                                                                                                                                      460
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dlukov B.C., Dunn P.,
RA Dodson K., Devangelista C.C., Ferrar C., Ferriera S., Fleischmann W.,
RA Dodson K., Evangelista C.C., Ferrar C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Ments S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Alasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Encese M.G.,
RA Alasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Encese M.G.,
RA Alasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Wilskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Weinstock S.M., Woodage T., Worley K.C., Wan D., Shun S., Zhon Q.A.,
RA Jaha R., Weinstock G.M., Weissenbach J.,
RA Jaha R., Weinstock G.M., Weissenbach J.,
Ra Jaha R., Weinstock G.M., Weinstock G.M., Smith H.O.,
Ra Jaha R., Shun B., Shun B., Shun B., Shun B., Shun B., Shun 
                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20196006; PubMed-10731132;
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00370; FGGY; 1
Pfam; PF02782; FGGY_C;
TIGRFAMS; TIGR01315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0035484;
                             188
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ADVCAQSVAGIGFDATCSLVVLDKNGDPLPVSPEGDAKQNIIVWMDHRATEQAERINATH
                                                                      HSLLKYVGGQVSLEMEVPKLLWLKRNLSQTFGNIWRVFDLPDFLTWRATGVDTRSLCSVV
                                                                                                   HPVLNYVGGKISPEMETPKILWLKENMPEIYERAGQFFDLADFLTWRATGDLARSVCTVT
                                                                                                                                                                    GGVDKSKVKGIGFDATCSLVVLGPQGSPLTVSKSGEAEQNIILWMDHRAEQETQEINAFK
                                                                                                                                                                                                                                                           VGVDVGTGSARAALVACDGRVLEQAVQTIQTWNPEPGYYNQSSDNIWQSICQVVKK--VI
                                                                                                                                                                                                                                                                                                       IGVDVGSGSVRAGIFDLNGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNALTL
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000577; FGGY_kin.
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                    59641 MW;
                                                                                                                                                                                                                                                                                                                                                                             35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5C_CHO_kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG11594.
                                                                                                                                                                                                                                                                                                                                                     Score 1005.5; DB 5;
Pred. No. 9.8e-62;
3; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    D934CAA8D72A0E6B CRC64;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                               125
                                                                                                                                                                                                                127
                                                                                                                                                                                                                                                              65
                          247
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                                                                                                                                                                                        Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin Houmiel K., Gordon J., Vaudin M., Hartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
                                                                                                          "Genome sequence of the plant Agrobacterium tumefaciens C58. Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chumley F.,
Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                      EMBL; AE009374; AAL45247.1; EMBL; AE008240; AAK88987.1;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=21608551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21608550; PubMed=11743193; Wood D.W., Setubal J.C., Kaul R., Monks D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATU4453 OR AGR_L_826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8U7J6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8U7J6
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Complete proteome 525 AA; 56072
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                                                                                                                                          pathogen . ";
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Rhizobiaceae group;
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Query Match Best Local Similarity

34.5%;

Score 971; DB 16; Pred. No. 2.3e-59;

Length

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submitted (OCT-2001) to the EMBL/GenBank/DDBJ
EMBL; BC014947; AAH14947.1; -.
InterPro; IPR000577; FGGY_kin.
Pfam; PF02782; FGGY_C; 1.
TIGRFAMS; TIGR01315; 5C_CHO_kinase; 1.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 439 AA; 47706 MW; 6DF2354474EBE3I
                                                                                                                                                                                                                                                                                           Q96C11 PRELIMINARY; PRT; 439 AA.
Q96C11;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 47.7 kDa protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                  TISSUE-SKIN;
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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           VWMDHRATEQAERINATHHPVLNYVGGKISPEMETPKILWLKENMPEI-YERAGQFFDLA 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGSAILGAVAGNIAPSV---GEAMQQ-----FTHVDKYYYPQERYQSLHHRRYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PG--VWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLDFHPAVEEAREMAQRVNQPLPVWLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIGLDTGCQVAAGMIDAYAGALGAL---GCCLAEDVGKHVALIAGTSSCLVAMSTQP--M
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MWLDHRAVSQVNRINETKHSVLQYVGGVMSVEMQAPKLLWLKENLREICWDKAGHFFDLP
                                                                Similarity
                                                   33.4%; Score 940; DB 4; Length 439; Ilarity 44.5%; Pred. No. 2.6e-57; Conservative 78; Mismatches 148; Indels
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                                                                                                                                                                                                                                                                       Primates;
                                                                                                                                                                                                                                                                                Chordata;
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                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                         6DF2354474EBE3E8
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                                                                                                         CRC64;
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Best Local S
Matches 210
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0960C2; Q7EMBLrel. 19, Creat
01-DEC-2001 (TrEMBLrel. 19, Last
01-JUN-2002 (TrEMBLrel. 21, Last
Conserved hypothetical protein.
61D6.030.
                                                                                                                                                                                                       German Neurospora genome project;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ
EMBL; AL513408; CAD11374-1; -
Interpro; IPR000577; FGGY_kin.
Pfam; PF00370; FGGY; 1.
TIGRFAMS; TIGR01315; SC_CHO_kinase; 1.
Hypothetical protein.
SEQUENCE 598 AA; 64896 MW; 9A91804D8270919
                                                                                                                                                                                                                                                                                                                                        Schulte U., Aign V., Hoheisel J., Brandt P., Nakatura G., Mewes H.W., Mannhaupt G.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                    Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5141;
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                                                                                                  DTCGIPVITTQCCEPVLLGSAILGAVAGNIAPSVGEAMQQFTHVDKYYYPQERYQSLHHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIGTVG--VEGGAL------NNLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DELTWRATGDLARSVCTVTCKWTWLAHENRWDPDYFRTIGLAELADEDFIRIGHHIVSPG
LAEAEKINNTNHNLLRYVGGKMSVEMEIPKVLWLKNNMPPELFARC-KFFDLTDALTYIA
                                                  VLAESKVDPNSVKGIGFDATCSLAVFTHDTN-EPVPVTGPDFKNDGN-DRNVILWLDHRP
                                                              ALTLADVCAQSVAGIGFDATCSLVVL--DKNGDPLPVS-----PEGDAKQNIIVWMDHRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RYEAY-KOLOHTAKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DITGMPVVLSQEVESVLVGAAVLGACASGDFASVQEAMAKMSKVGKVVFPRLQDKKYYDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLKLSQDLDDLAILYLATVQAIALGTRFIIEAMEAAGHSISTLFLCGGLSKNPLFVQMHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVKATARCQSIYAYLNSHLDLIKKAQP--VGFLTVDLHVWPDFHGNRSPLADLTLKGMVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASLGNGLTPEAARDLGLLPGIAVAASLIDAHAGGLGVIGADVRGHGLICEGQPVTSRLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFLSWKATGVTARSLCSLVCKWTYSA-EKGWDDSFWKMIGLEDFVADNYSKIGNQVLPPG
                                                                                                                                                                    Similarity
                                                                                                                                                         Conservative
                                                                                                                                                      31.6%; Score 887; DB 3; Length 598; 36.3%; Pred. No. 1.9e-53; tive 105; Mismatches 204; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                          9A91804D82709195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                    Fartmann
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                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                   В.,
                                                                                                                                                                                                                                                                                                                                                                    Holland
                                                                                                                                                         60;
                                                                                                                                                       Gaps
                                                   126
 185
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Best Loc
Matches
                                                                                                                                                        InterPro; IPR000577; FGGY_kin.
Pfam; PF00370; FGGY; 1.
TIGRFAMs; TIGR01315; 5C_CHO_kinase;
                                                                                                                                                                                                                                                                                                                                                                      Q04585 PRELIMINARY; PRT; 715 AA. Q04585; O1-NOV-1996 (TrEMBLrel. 01, Created) O1-NOV-1996 (TrEMBLrel. 01, Last sequence up 01-JUN-2002 (TrEMBLrel. 21, Last annotation Hypothetical 79.2 kDa protein.
                                                                                                                                                                                        Barrell B., Rajandream M.A., Submitted (MAR-1995) to the EMBL; Z48758; CAA88663.1; -. SGD; S0002516; YDR109C.
                                                                                                                                                                                                                                                                     Murphy L., Shore L.,
Submitted (MAR-1995)
                                                                                                                                    Hypothetical protein. SEQUENCE 715 AA; 7
                                                                                                                                                                                                                                     STRAIN-AB972;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-AB972;
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharon Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                                 Local 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544
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                                                                  G
KFYVGVDVGTGSARACVIDOSGNMLSLAEKPIKREQLISNFITQSSREIWNAVCYCVRTV
                                                      KTVIGVDVGSGSVRAGIFDLNGSLLSHATEKITTTRRSGSRVEQSSQEIWQAVCSCIRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGDLARSVCTVTCKWTWL-----AHENRWDPDYFRTIGLAELADEDFIRIG------HII
                    LTLADVCAQSVAGIGFDATCSLVVLD-KNGDPLPVSPE-GDAKQNIIVWMDHRATEQAER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKPGKTVWSRGDPAEK--KLLDAKYEIFLDQARTQQEYR 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THVDKYYY----PQERYQSLHHRRYEAYKQLQHTAKLLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGQHPLVRQILADTCGIPVITTQCCE-PVLLGSAILGAVAGNIAPS-----VGEAMQQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPIADPNMRGAIIGMSNDKSKDGMALLYYSTMEFIALQTRQIVEAMNTAGHTIKSIFMSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSAGELVG-GLSEEAGQQLGLPAGIAIGSGVIDAYAGWIGTVGAKVKLSPDHRDDSVAPN
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                                                                                                   Similarity
                                                                                        Conservative
                                                                                                                                    79160 MW;
                                                                                                  30.8%;
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to the
                                                                                        100;
                                                                                                 Score 864.5; DB 3
Pred. No. 9.1e-52;
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EMBL/GenBank/DDBJ
                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                           Walsh
                                                                                                                                                                                                                                                                                                                                                  Saccharomycotina; Saccharomycetes;
                                                                                                                                   A52B2D9B4B4C9C7E CRC64;
                                                                                        Mismatches
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                                                                                                                                                      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
A. Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
A. Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
A. Nunco J., Pacleb J., Paradas V., Park S., Phouanenavong S., Wan K.
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AV660286; AALJ5325.1; -
RR FlyBase; FBgn0035484; CG11594.
R FlyBase; FBgn0035484; CG11594.
R InterPro; IPR000577; FGGY_kin.
R FIGRFAMS; TIGR01315; 5C_CHO_kinase; 1.
R SEQUENCE 439 AA; 48172 MW; F26903DBB321A40E CRC64;
                                                                                                                 Query
Best I
                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q95T84;
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01-DEC-2001
01-JUN-2002
GH12991p.
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoá; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                     STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
              172
                                                                       112
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MDHRATEQAERINATHHPVLNYVGGKISPEMETPKILWLKENMPEIYERAGQFFDLADFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HARAVICGLGMERDLDNLLALYIAGLCGIGYGLRQILDAQTAQGVVSKNIVISGGAGQHP
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                                           MDHRAEQETQEINAFKHSLLKYVGGQVSLEMEVPKLLWLKRNLSQTFGNIWRVFDLPDFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISPLDKKAACQLGLTEHCVVSSGIIDAYAGWVGTVAAKPESAVKGLAETENYKKDFNGAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCTVTCKWTWL-----AHENRWDPDYFRTIGLAELADEDFIRIG------HHIVSPGTPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INSSGDKCLKYVGGQMSVEMEIPKIKWLKNNLEAGIFQDCKFFDLPDYLTFKATGKENRS
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                                                                                                    167;
                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                      FROM
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                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                   N.A.
                                                                                                                27.4%;
37.9%;
                                                                                                    69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
                                                                                                                 Score 769.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                          Tracheata; Hexapoda; Insecta;
ota; Diptera; Brachycera; Musc
                                                                                                    Mismatches
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                                                                                                                   1.8e-45;
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                                                                                                                               DB 5;
                                                                                                    176;
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                                                                                                    Indels
                                                                                                                               Length
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Q9HA63
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ID O7HA63
AC O9HA63
AC OPHA63
AC
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IC TISSUE-MAMMARY GLAND;

IX ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

IA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

IA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

IA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

IA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

IA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

IA Ninomiya K., Iwayanagi T.;

I NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE 246 AA; 26576 MW; 04D5374635B4DB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 127; Conserv
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ12175 fis, clone MAMMA1000713, weakly similar L-ribulokinase (EC 2.7.1.16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                              110 VWMDHRATEQAERINATHHPVLNYVGGKISPEMETPKILWLKENMPEI-YERAGQFFDLA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 EFHNRKYKVFLQLLENQRQYR 431
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279 VFGTSSCTMASTTSPSFVPGVWGPYYSAMVPGLWLVEGGQSAAGAAIDQLLDFHPAVEEA 338
                                                                                                                                     229 TPCGNGLTAQAAAEMGLLPGTPVAVGLIDAHAGGIGTVG---VEGGAL------NNLAY 278
                                                                                                                                                                                                                                                      169 DELTWRATGDLARSVCTVTCKWTWLAHENRWDPDYERTIGLAELADEDFIRIGHHIVSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVITGLDMTRGTESLAIKYLAFVQALAYGTRHIIENLYQYGRAPFQTLLFCGGLAKNPLY
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                                                                                          ASLGNGLTPEAARDLGLLPGIAVAASLIDAHAGGLGVIGADVRGHGLICEGQPVTSRLAV
                                                                                                                                                                                                                      DFLSWKATGVTARSLCSLVCKWTYSA-EKGWDDSFWKMIGLEDFVADNYSKIGNQVLPPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.9%; Score 672; DB 4; Length 246; 52.0%; Pred. No. 4.8e-39; tive 38; Mismatches 67; Indels
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Db 180 ICGTSSCHMGISKDPIFVPGVWGPYFSAMVPGFWLNEGGQSVTGKLIDHMVQGHAAFPEL
QY 339 REMA 342
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Search completed: March 13, 2003, 16:55:12 Job time: 37.0381 secs

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Perfect score:
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AAE09781
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AAB18235
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ABB47287
ABB53425
AAY023610
AAB98023
AAB84207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             908470
                                                                                                                                                                                               Description
                                                                                                        Staphylococcus epi
C glutamicum prote
Chlamydia trachoma
                Amino acid sequenc
Pseudomonas mendoc
                                                                        Enterococcus faeca
                                                                                                                                                              Escherichia coli s
                                                    Lactococcus lactis
                                                                                       Plasmodium
                                                                                                                                                                                                                                                                                                      to have a being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . DAT: *
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Group B Streptococ	AAY91291	21	401	5.8	129
trepto	ABP29844	23	400	5.8	129
Streptococcus poly	791	23	400	5.8	129
C glutamicum prote	AAG93123	22	453	5.9	129.5
C glutamicum prote	AAG92442	22	, 701	5.9	130
	AAB35474	22	518	5.9	130
	ABB66844	22	542	5.9	130.5
lacti	ABB53687	23	467	5.9	130.5
Escherichia coli p	ABB52555	22	466	5.9	131
Streptococcus poly	ABP27912	23	433	5.9	131
Salmonella enteric	AAW88344	20	430	6.0	132
Staphylococcus epi	ABP40365	23	423	6.0	132.5
. C. glutamicum SRT	AAB78973	22	412	6.0	132.5
Corynebacterium gl	AAB76763	22	402	6.0	132.5
C glutamicum prote	AAG92975	22	, 378	6.0	132.5
Streptococcus poly	ABP30110	23	490	6.0	133.5
aphylococcus	ABP40002	23	492	6.2	136
coli growth	AAG98958	22	425	6.2	136.5
E. coli cellular p	AAU34874	22	425	6.2	136.5
Lactococcus lactis	ABB53977	23	405	6.2	137
Listeria monocytog	ABB47392	23	382	6.2	137
Escherichia coli p	ABB52906	22	454	6.2	138
Staphylococcus car	AAW26740	18	388	6.2	138
	AAG92801	22	449	6.3	138.5
S	AAU34999	22	417	6.3	139
	AAB84873	22	447	6.3	140
Lactococcus lactis	ABB54015	23	496	6.4	141
Chlamydia pneumoni	AAY35284	20	352		141
Drosophila melanog	ABB60537	22	, 497		142
C glutamicum prote	AAG93189	22	595		143.5
Corynebacterium gl	AAB76735	22	484		143.5
Staphylococcus epi	74	23	393		145
	31	23	401		147
seudomonas stutz	E0585	22	392	6.9	
Streptococcus poly	ABP28804	23	397		155

ALIGNMENTS

AAE09781;

AAE09781 standard; Protein; 424 AA.

RESULT 1 AAE09781 ID AAEC XX AAE AC AAEC XX AAEC XX POS: KW POS: KW rib: XX FOS XX POS XX POS XX BSC] XX POS XX IBXX AAEC XX POS XX POS XX POS XX POS XX POS XX POS XX W02(XX POS XX W02(XX POS XX W02(XX W02(XX W02(XX W02(XX W02(XX W02(XX W02(XX W02(XX W02(XX W02(XX W02(XX W02(XX W02(XX W02(XX W01) XX W01 XX W01 XX W01 DR W01 D WPI; 2001-565596/63. N-PSDB; AAD16811. Positive selection system; metabolise; arabitol; ribitol; mannitol; transgenic cell; marker gene; ribitol dehydrogenase; ribitol kinase ribitol transporter; rtl operon. 08-MAR-2000; 15-AUG-2000; 08-MAR-2001; 2001WO-US07474 Escherichia coli C. 29-NOV-2001 (first entry) Positively selecting transformed cells comprising selectable marker Parrott W, 13-SEP-2001 WO200166779-A2. Escherichia coli strain C rtl operon encoding ribitol transporter. (UYGE-) UNIV GEORGIA RES FOUND INC. Lafayette 20000S-0188291. 20000S-0255595. P, Kane ۳,

Amino acid sequenc

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ABP38175
ID ABP3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc involves conferring to transferred cells the ability to metabolise cc arabitol, ribitol and/or mannitol. The positive selection method is cused in positively selecting transgenic cells from a population of cells cc used in positive selection method, the presence of the gene of cells interest in the genetically transformed cells may be determined without the disadvantages associated with traditional negative selection cc systems. Positive selection of the transformed cells is achieved without creatly damaging the neighbouring non-transformed cells. The cuse of a separate assay to determine the presence of a marker gene. This technique also avoids the release of antibiotics or other dangerous genes into the environment. The present sequence is Escherichia coli strain C ribitol transporter encoded by ribitol operon (rtl operon). The operon also encodes ribitol dehydrogenase and ribitol kinase.
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e.g., ara
cells -
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 Staphylococcus antibacterial;
                                           Staphylococcus
                                                                                                                                ABP38175 standard; Protein;
                                                                                                     ABP38175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSAGMSNFLAPAIAVVLLPWFSTIGVVIAYTALYLLAFVLCAFIRVEQPGFSSAPVTEKA
                                                                                                                                                                                                                                                                                                                                  GMAASSLAFYYMPQYFGHNYWMAMIPATALGTFVAAFVPMAAVFPALEPKHKGAAISVYN
                                                                                                                                                                                                                                                                                                                                                                                            LFGFAVIMPMMFVDELGFTTSEWLQVWAAFFFTTIFSNIFWGIVAEKMGWMRVIRWFGCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNIS
                                                                                                                                                                                                                                                             LSAGMSNFLAPAIAVVLLPWFSTIGVVIAYTALYLLAFVLCAFIRVEQPGFSSAPVTEKA
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                                                                      (first entry)
epidermidis;
gene therapy
                                           epidermidis ORF
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                open
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Pred. No. 3.
                                           amino acid sequence SEQ
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                reading
                frame;
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                ORF;
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                bacterial infection;
                                           ID NO: 3020.
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-1997;
08-NOV-1997;
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                                 LAPAIAVVLLPWFSTIGVVIAYTALYLLAFVLCAFIRVEQP
                                                                                                                                                                     MMFVD-ELGETTSEWLQVWAAFFFTTIFSNIFWGIVAEKMGWMRVIRWFGCLGMAASSLA
                                                                                                                                                                                                                                               MISLRHVKTPGHMHNLTPREKFAELSRAVTLLYTNRNIFLSSIVRIINTLSLEGEAVIMP
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DB; ABN90720.
                                                                                                           FYYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAVFPALEPKHKGAAISVYNLSAGMSNF
                                                                                                                                                                                                                          MYLVKERGAGKPDDAVTLVERLKTLSSGVTIIAERRGMFLIVLVRIICNLSLFGLPVILP
                                                                                                                                                                                                                                                                                                                                                                          VLAETFGPRRIMLIGVAAWIVFHVLFLIFGLEQQKYTLMVVFYGIRGLAYPLFIYAFMVW
                                                                        FYYLPQFYGAHFEIALIAAIGFGISVTAFVPMGAVFLALAPEQKGAAISAHNLAAGLSNF
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195; Conser
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97US-064964P.
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Pred. No. 3.3e-102;
6; Mismatches 129;
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the executive of the first sequence is a protein described in the executive of the first sequence is a protein described in the executive.
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Tateishi N,
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                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                           in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; SEQ ID NO: 3627; 246pp + Sequence Listing; English
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SLIALLGVKE-RRGRHPLVANPDDVKQTLGQGFKLLRNDRRARFVTYIRTINSIPTYAMA
                              GVIAMISLRHVKTPGHMHNLTPREKFAELSRAVTLLYTNRNIFLSSIVRIINTLSLFGFA
                                                             VWITATASPKQLGTGVGWFYVAFSAGLPTLGALVATISMQYVNLTFYETLWVSLVLVVIG
                                                                                            VVIIHNVRSENSSSALGWYWAVYSVGIGVAGSYIPSFTIPIMG--EMGTLWLALAFCFAG
                                                                                                                           AAALSDLWGPRKVMILGASIWIVFELIFLTVALTTDHTWLIFLAYGLRGFGYPFFAYGFL
                                                                                                                                         SGVVAEIITPQKTMLIGFVLWCVFHVLFLVFGLGQANYGLILLFYGIRGLAYPLFLYSFI 127
                                                                                                                                                                                     LGIPRPLIFGFIGLTIFMIGDGVETNILEPFLSSEHGFSVSLAGTLVTVYGVAVAIAAFF
                                                                                                                                                                                                                    LGLPLHLIWGYIAIAVFMTGDGFELAFLSHYIKS-LGFTPAEASFAFTLYGLAAALSAWV
                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                               Patent Office
                                                                                                                                                                                                                                                                                                                 445 AA;
                                                                                                                                                                                                                                                     Conservative
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2000JP-0280988.
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da M,
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Pred. No. 3.8e-53;
                                                                                                                                                                                                                                                     Mismatches
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Ozaki A;
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                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                     188;
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                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                  Length 445;
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28-NOV-1997;
17-DEC-1997;
                                                                                            can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention
                                                                                                                                                                                             AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                           Griffais
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia trachomatis transport
                                                                                                                                                                                                                                                                                  Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9928475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY37671 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246
                                                                                   be of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIMPMMEVDELGETTSEWLQVWAAFFETTIFS----NIFWGIVAEKMGWMRVIRWEGCL
                                                                                                                                                                                                                                                                                                               1999-371125/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPALAEDAHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFFPSFFTDDL-----KWQLSWFLILTTVIYAVNLPFNPFFGSFGDRHGWARTVFWGGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAPVTEKALNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAMATYNLGVGGAVAVGPLLVAVFHPLIGPTGLILVMIALYLLSGWMTLQLRGTQPGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAISVYNLSAGMSNFLAPAIAVVLLPWFSTIGVVIAYTALYLLAFVLCAFIRVEQPGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAYTLALVYFIPM-FGVQAGMSNGVVFGITIAAGALFGVSLAGFVPLSAIAVSLDPKHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GMAASSLAFYYMPOYFGHNYWMA------MIPAIAL-GTFVAAFVPMAAVFPALEPKHK
                                                                                                                                                                                                                                                                                                                                          æ
                                                                                  use in
                                                       414
                                                                                                                                                                                                                                                      Page 1298-1300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                   97FR-0016034
                                                                                                                                                                                                                                                                                                                                                                                                               98US-0107077
97FR-0015041
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-IB01939
                                                                                  treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
           7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conventional trachoma;
                                                                                                                                                                                                                                                     1755pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414
Score 174.5; DB 2
Pred. No. 7.5e-10;
3; Mismatches 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                           DB 20; / Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nonendemic trachoma;
                           414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424
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Matches

Local

Similarity 98; Conser

Conservative

63;

Indels

119;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                      (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                              Disclosure;
                                                  Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                            Plasmodium falciparum;
                                                                                                                                                                                                                                                                                                                                  Plasmodium
                                                                                              WPI; 2000-365347/31
                                                                                                                   Hoffman
                                                                                                                                                                                           05-NOV-1998;
                                                                                                                                                                                                                05-NOV-1999;
                                                                                                                                                                                                                                    11-MAY-2000
                                                                                                                                                                                                                                                          WO200025728-A2
                                                                                                                                                                                                                                                                               Plasmodium falciparum
                                                                                                                                                                                                                                                                                                  antimalarial; malaria;
                                                                                                                                                                                                                                                                                                                                                       07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                             AAB18235;
                                                                                                                                                                                                                                                                                                                                                                                                AAB18235 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVALLACALI 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRGPMNVV---FSLGLLVSILGLWGTRDYF--VWWIDGTFLFIIGFFL--FGPQMMIGLA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLAFVLCAFI 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REKFAELSRAVTLLYTNRNIFLSSIVRIINT------LSLFGFAVIMPMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GL-SSTIPLFVLFWGINGWFQGWGWPPCARLLTHWY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAELSHKKAA----GTASGFTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KMGWMRVIRWFGCLGMAASSLAFYYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAV-FP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVND------WSALYLIETKDYSTVKANLCVSLFEIGGLFGMLLAGWLSDTISKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVDELGETTSEWLQVWAAFF-----FTTIFSNI-----FWGIVAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STSHNIGGALIPVLTGVAIDYTGWRGVMFIPGIICIIMGFILIDRLR--DTPQSL-GLPA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLGQANYGLILLFYGI----RGLAYP----LFLYSFIVVIIHNVRSENSSSALGWYWAVY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IADLGFDKAQLGIIGSTLY-ITYGISKFVSGVMSDQSNPRYFMAIGLIITGISNIF---F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKSLGETPAEAS-FAETLYGLAAALSAWVSGVVAEIITPOKTMLIGFVLWCVFHVLFLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IEKFRKEEDAHPHEETTADILEEEAERELSTKEILFTYVLSNKWLWFLSFASFFIYVVRM
                                                                                                                   Ś
                                                                                                                                                                                                                                                                                                                                falciparum chromosome 2 related
                           Page 220-221; 577pp; English
                                                                                                                   Carucci
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                               99WO-US26796
                                                                                                                                                                                           98US-0107131
                                                                                                                   'n
                                                                                                                                                                                                                                                                                                  chromosome 2;
protozoacide;
                                                                                                                  Gardner M,
                                                                                                                                                                                                                                                                                                                                                                                                457
                                                                                                                                                                                                                                                                                                                                                                                                ₿
                                                                                                                  Venter
                                                                                                                                                                                                                                                                                                  human malaria parasite; vaccine;
infection; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -WFAYFGAAFAGYPLGKVAQDWGWHGF
                                                                                                                  JC
                                                                                                                                                                                                                                                                                                                                 protein SEQ ID NO:92
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                                                          parasite,
and in th
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum.

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RESULT 6
ABB47287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2) CC vaccines against P. falciparum infection comprising (I) or (II). CC (I) and (II) are useful for the development of vaccines against CC P. falciparum infection. (I) and polyclonal antisera or a monoclonal CC antibody raised to immunogens comprising the sequences of (I), are CC useful in the detection of infection with P. falciparum. Furthermore, CC (I) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent P. falciparum CC infection, or they can be used to identify drug resistance in CC p. falciparum. Sequencing of the Plasmodium chromosome 2 and the CC subsequent identification of proteins encoded by it will help to expand CC our understanding of parasite biology, a process hampered by the CC complexity of the parasite biology, a process hampered by the CC vaccine and drug development. Parasite resistance to drugs and mosquito CC resistance to insecticides have led to a resurgence of malaria in many CC parts of the world, and there is a pressing need for vaccines and new CC crossitance to AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not conscient and within the present invention, but which are not conscient and within the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 90
                Enterococcus faecalis
                                                      MDR; efflux pump; multidrug
                                                                                                                                        31-JAN-2002
                                                                                                                                                                                                                        ABB47287 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specifically mentioned within the specification.
                                                                                                Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 FLSHYIKSLGFTPA---EASFAFTLYGLAAALSAWVSGVVAEIITPQKTMLIGFVLWCVF 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 HVL--FLVFGLGQANYGLILLFYGIR-----GLAYPLFLYSFIVVIIHNVRSENSSSALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 YVISYMKIIGCSDVKYKDSSWIYVLTLLFQCFFGFFGGILNQNLGPQISVLLGGWLMCLG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VISGIIFIGRGLSVFIICPLQNYYINKYNYMPDYMPEIENSDEKYFSNLDILNKVPYLFI
                                                                                                                                                                                                                                                                                                                                                               MSNFLAPATAVVLLPWFSTIGVVIAYTALYLLAFV 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLRTLSNTSNESEREV------NNTFINREFILIWLMIFFNWQAISYTQVFWKIFGMNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALAFCFAGGVIAMISLRHVKTPGHMHNLTPREKFAELSRAVTLLYTNRNIF-----LSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WYWAVYSVGIGVA-----GSYIPSF-----TIPIMGEMGTLWL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSIDDRSLSLLGSVSSLFNIFGRIFWGLISDFTSFKTTLILMSLLMSF--LTITLTMSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEGICFA--IIQFLGSYLIADSGD----TSKDFMAYNDRNNKVLYFEEKNFINKPNGLSN
                                                                                                                                                                                                                                                                                                                         FSSIINAIISAVLL---NNIGNIAMCAIVSLSSFV 449
                                                                                                                                                                                                                                                                                                                                                                                                         YGIITY---SIWVCLIFFCHAGTF-----AIFPSITAHTFGTKNFGPVFGLLFTARA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                               YYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAVFPALE-----PKHKGAAISVYNLSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVRIINTLSLEGEAVIMPMMEVDELGETTSEWLQVWAAFFET----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.6%;
nilarity 19.8%;
Conservative 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 AA;
                                                                                            faecalis polypeptide NorA
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TIFSNIFWGIVAEKMGW-----MRVIRWFGCLGMAASSLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;; Score 168.5; DB 2
;; Pred. No. 3.8e-09;
78; Mismatches 154
                                                                                                                                                                                                                          394
                                                        resistance; antibacterial;
                                                                                                                                                                                                                          AΑ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
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                                                        drug target
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RESULT 7
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to determining whether a candidate nucleotide (ABA82938-ABA82971) or polypeptide (ABA9236-ABB47296) encodes/functions as a multidrug resistance (MDR) efflux pump comprising, searching a database for sequences high identity known MDR efflux pumps and then deleting/mutating an identified region of the DNA in a bacterial cell and determining whether the bacterial cell exhibits increased or decreased sensitivity to an antibacterial agent The identified pumps are useful for further identifying MDR efflux pumps that may be used as drug targets to increase the sensitivity of cells to antibacterial agents. Cells comprising the identified pumps may be used to screen for potential blockers or inhibitors of MDR pump function or gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining whether a candidate nucleotide or polypeptide encodes/functions as a multidrug resistance (MDR) efflux j searching a database of nucleotide/polypeptide sequences high identity to known MDR pumps -
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                                                                                                                                AAISVYN----LSAGMSNFLAPAIAVVL-----LPWFSTIGVVI--AYTALYL
                                                                                                                                                                                               AASSLAFYYMPQYFGHNYWMAMIP----AIALGTFVAAFVPMAAVFPALE---PKHKG
                                                                                                                                                                                                                                                              FAVIMPMMFVDELGFTTSE-WLQVWAAFFFTTIFSNIFWGIVAEKMGWMRVIRWFGCLGM
                                                                                                                                                                                                                                                                                             LTLTVLKE-----PEKRILAAVEAKKGSFMDILRNPMFTSLFVIILISSFGLQA
                                                                                                                                                                                                                                                                                                                                                           DMTTISERPKAMGLVSAAISGGFIIGPGVGG-----FIAYLGIRAPFFAAAFLAFIGFI
                                                                                                                                                                                                                                                                                                                                                                                            HNVRSENSSALGWYWAVYS----VGIGVAGSYIPSFTIPIMGEMGTLWLALAFCFAGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITPQKTMLIGFVLWCVFHVLFLVFGLGQANYGLILLFY---GIRGLAYPLFLYSFIVVII 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLAISNLFLVFL-GVGLVIPVIPQLKEEMHFSGTTMGMMISIFAIAQLITSPIAGVLSDK
                                                                                                  DQQGTINGLNSTFTSFGNILGPMAAGALFDINHFFPYYVSAVILLGTGFLSLFL
                                                                                                                                                                                                                                FESIYSIMATINFGFTTSEIAIVITVSGILALICQLFFFDAIVQKIGEMGLIQL-----
                                                                                                                                                                                                                                                                                                                             IAMISLRHVKTPGHMHNLTPREKF--AELSRAVTLLYTNRNIFLSS--IVRIINTLSLFG
                                                                                                                                                                                                                                                                                                                                                                                                                            IGRKKMIATGML---VFSISELLFGLAQAKSG----FYISRGLGGIAAALLMPSVTAFVA
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                  standard;
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                                                                                                                                                               TFFASAIFIAVIAFTKNNLVVVFSTFI-VFLAFDLFRPAVTTYLSKHAG
                Protein;
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                  387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention helps research in lactic bacteria, particularly production of yogurt and cheese.

Note: The sequence data for this natery to bear a first the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleotide sequence useful lactis and related, species -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-2000;
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LE---PKHKG---AAISVYNLS-AGMSNFLAPAIAVV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSAWVSGVVAEIITPQKTMLIGFVLWCVFHVLFLVFGLGQANYGLILLFY---GIRGLAY 119
                                                                                  LIQL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLFLYSFIVVIIHNVRSENSSSALGWYWAVYS----VGIGVAGSYIPSFTIPIMGEMGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNKKSMMNLAISNLF-----LVFL-GAGLVIPVLPTLKEQMHFSGTTMGMMISIFAIAQL
                                                                                                                                                                                                                                         RIINTLSLFGFAVIMPMMFVDELGFTTSEWLQVWAAFFFTTIFSNIF-WGIVAEKMGWMR
                                                                                                                                                                                                                                                                                             YVAAILAFLGFILTITILKEPERTIESHQEIEKVSFLDIL-----
                                                                                                                                                                                                                                                                                                                                            WLALAFCFAGGVIAMISLRHVKTPGHMHNLTPREKFAELSRAVTLLYTNRNIFLSS--IV
                                                                                                                                                                                                                                                                                                                                                                                                      AMLMPSVTAYVADMTTIAERPKAMGLVSAAISGGFIIGPGV-GGFIAHFGIRV-----PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VASPVAGALSDKIGRKKLIAIGMI - - - IFSFSELLFGLAQAKTG - - -
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21.0%;
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                              -LLPWFSTIGVVI - - AYT
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                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                  from Pseudomonas mendocina KR-1. The protein increases resistance to solvents and antibiotics, and is used particularly for constructing strains that produce p-hydroxybenzoic acid. Overexpressing the efflux system or its expression from a plasmid vector increases resistance of bacteria to a variety of toxic substances, while inactivating an efflux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 32-33;
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                                                                                                                                                                                                                                                                                                                                                           system increases sensitivity to antibiotics and toxic substances
                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a putative efflux protein obtained from Pseudomonas mendocina KR-1. The protein increases resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative efflux protein; Pseudomonas mendocina KR-1; solvent; antiblotic; p-hydroxybenzoic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316
 235 IINTLSLFGFAVIMPMMFVD---
                                                                                                                                                                                64
                                                                                                                                                                                                            66
                                                                                                                                                                                                                                       20 IAIAVEMTG-----DGFELAFLSHYIKSLGFTPAEASFAFTLYG------LAAAL
                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      putative efflux protein gene increases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-313345/26
DB; AAX59540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLFL
                                                                                                                  LFLYSFIVVIIHNVRSENSSSALGWYWAVYSVGIGVAGSYIPSFTIPIMGEMGTLWLALA
                                                                                                                                                  AVW-----LTPKVGGGRMIAASGAVCALALLLIPLSSNTFVIGVLLTL--LAGTAAT
                                                                                                                                                                             SAWVSGVVAEIITPQ----KTMLIGFVLWCVFHVLFLVFGLGQANYGLILLFYGIRGLAYP
                                                                                                                                                                                                          VAVVVLLTGLVAATYGFGIYLFAQLVPDM----QASLGFGFSYVGTITASAQLGFLLCAML
                            LLTLAMTVLVLVVL----KRGGLLGQALPSAPTATTDEAAS-----SSGLSGLIRPWVLL
                                                        -FCFAGGVIAMISLRHVKTPGHMHNLTPREKFAELSRAVTLLYTNRNIFLSSIVR----
                                                                                        VFV-PMVDVIARVVAYRYRGLAMGLVSSGTSYGVAINSLLVPIYA--PQGEWRSVWWVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTTYLSKHAGNRQGAINGLNSAFTSFGNILGPMAAGYMFDLNHLFPYYISAIILLGTGFL 375
                                                                                                                                                                                                                                                                  Similarity 22.7
88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379
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                                                                                                                                                                                                                                                                                                                              416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28pp;
                                                                                                                                                                                                                                                                                   7.28; 22.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             putative
                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416
                                                                                                                                                                                                                                                                  Score 158.5; DB 20;
Pred. No. 3.9e-08;
8; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          င္ပ
 - ELGFTTSEWLQVWAAFFFTTIFSNIFWGIVAEKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Ŧ)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           efflux protein.
                                                                                                                                                                                                                                                                                                 DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         solvents
                                                                                                                                                                                                                                                                                                 416;
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                                                                                                                                                                                                                                                                  Gaps
 289
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                            Pseudomonas efflux proteins in the transformed host cell relative to expression levels of an untransformed host cell. (I) is useful for isolating cDNAs and genes encoding a homologous putative efflux 4.5x gene from the same or other bacterium species. (I) is useful as a restriction fragment length polymorphism (RFLP) marker, and for carrying out nucleic acid amplification-based methods of genetic and physical mapping. (I) is useful for probing an organism's efflux system to gain an understanding of the mechanism of solvent tolerance.
                                                                                                                                                                  The present sequence represents a putative efflux protein, designated 4.5x, isolated from Pseudomonas mendocina KR-1. The putative efflux 4.5x gene (I) is located immediately downstream of the pobA gene in Pseudomonas mendocina KR-1. The present invention also describes: (1) a chimeric gene (II) comprising (I) operably linked to at least one suitable regulatory sequence; (2) a transformed host cell (III) comprising (II); (3) isolation of (I); and (4) a complement of (I). (II) is useful for altering the level of expression of Pseudomonas efflux protein in a host cell by transforming the cell with (II), and growing the transformed host cell produced under conditions that are suitable for expression of (II), resulting in production of increased levels of
                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated Pseudomonas efflux polynucleotide, useful for probing organism's efflux system to gain understanding of the mechanism of solvent tolerance and as restriction fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen KK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         solvent tolerance.
                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-342396/36.
N-PSDB; AAH21716.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB98023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-OCT-1998;
31-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restriction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSKLASSSAMAVSIFGIANVMQGSGGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPK---HKGAAISVYNL----SAGM 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IWSMNFLIGFATFPFQTYLSSYLRTELGFDVQYTAQVWAVIGFVGMFAGLAVGWLSDRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LRFAMYLVYGCVVTAA--LIFVVQPS--GH--W----PLVAAVLFSTAFYPIFGLIPAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WMRVIRW--FGCLGMAASSLAFYYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAVFPAL
                                                                                                                                                                                                                                                                                                                                                                            Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment length polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mendocina
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97US-0961738.
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                                                                                                                                                                                                                                                                                                                                                                            23-26; 17pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KR-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFLP marker; genetic mapping;
marker; physical mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO:2
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Sequence

416 AA

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RESULT 10
AAB84207
ID AAB844207
ID AAB844207
ID AAB844
XX O6-AU
XX Efflu
XX Efflu
XX Efflu
XX Pseud
XX Pseud
XX 15-JU
XX 15-JU
XX 10UPC
XX 10UPC
XX WPI;
DR WPI;
DR WPI;
DR W-PSI
XX VPI Soli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      US6235882-B1
                                                                                                                                                                                                                                                                                                                                                                                                                              Efflux 4.5x protein; Pseudomonas mendocina KR-1;
The present sequence represents a putative efflux 4.5x protein. I isolated from Pseudomonas mendocina KR-1. Efflux proteins play an important role in bacteria by conferring resistance to toxic comp
                                                                                                 New gene encoding a putative efflux protein isolated from Pseudomonas mendocina, useful genes encoding a homologous putative efflux
                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-2001
                                                                                                                                                               WPI; 2001-366425/38
N-PSDB; AAF90209.
                                                                                                                                                                                                                                                                 30-OCT-1998;
31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                          22-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a putative efflux gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB84207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB84207 standard;
                                                           Claim
                                                                                                                                                                                                                                    (DUPO)
                                                                                                                                                                                                                                                                                                             15-JUN-1999;
                                                                                     bacterial species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSKLASSSAMAVSIFGIANVMQGSGGM 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPK---HKGAAISVYNL-----SAGM 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LRFAMYLVYGCVVTAA--LIFVVQPS--GH--W----PLVAAVLFSTAFYPIFGLIPAY 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IINTLSLFGFAVIMPMMFVD-----ELGFTTSEWLQVWAAFFFTTIFSNIFWGIVAEKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLTLAMTVLVVL---KRGGLLGQALPSAPTATTDEAAS-----SSGLSGLIRPWVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -FCFAGGVIAMISLRHVKTPGHMHNLTPREKFAELSRAVTLLYTNRNIFLSSIVR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFV-PMVDVIARVVAYRYRGLAMGLVSSGTSYGVAINSLLVPIYA--PQGEWRSVWWVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVW------LTPKVGGGRMIAASGAVCALALLLIPLSSNTFVIGVLLTL--LAGTAAT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAWVSGVVAEIITPQ---KTMLIGFVLWCVFHVLFLVFGLGQANYGLILLFYGIRGLAYP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAVVVLLTGLVAATYGFGIYLFAQLVPDM----QASLGFGFSYVGTITASAQLGFLLCAML 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WMRVIRW--FGCLGMAASSLAFYYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAVFPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IWSMNFLIGFATFPFQTYLSSYLRTELGFDVQYTAQVWAVIGFVGMFAGLAVGWLSDRTG
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                                                        Column 21-24; 16pp; English
                                                                                                                                                                                                                                       PONT
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97US-0961738
                                                                                                                                                                                                                                                                                                             99US-0333254
                                                                                                                                                                                                                                     DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
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22.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164;
                                                                                                 for solvents or antibiotics for isolating cDNAs and 4.5x gene from other
                                                                                                                                                                                                                                                                                                                                                                                                                                toxic compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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 to toxic compounds
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                             Ιt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347
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RESULT 11
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                                                                                27-OCT-2000; 2000GB-0026333
24-NCV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus polypeptide
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                                                                                                                                                                                                     29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                                                                                             02-MAY-2002.
                                                                                                                                                                                                                                                                                                                    WO200234771-A2
                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP28804 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVW------LTPKVGGGRMIAASGAVCALALLLIPLSSNTFVIGVLLTL--LAGTAAT 172
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22.7%;
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Pred. No. 3.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cc streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS cc (Streptococcus/GBS (Streptococcus byogenes), comprising one of 5483 sequences (S1), given in ct the specification. The proteins have antibacterial and antiinflammatory cartivity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and cantibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Cc. Nucleic acids encoding (I) are used to detect Streptococcus in a cc. biological sample. (I) is used to determine whether a compound binds to cc. (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Cc. Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity corrections profering streptococcus professes, and distinguishing/identifying cr.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 3841; 4525pp;
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                                                                                                AVFPALEPKHKGAAISVYN-LSAGMSNFLAPAIAVVLLPWFSTIGVVIAYTALY----LL
                                                                                                                                                                                                    TSMITQISAQSV---APIL-SLYIRHLGQTHNLMFTSG---LVVSAMGFSSLFSSSYLGK
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                                                                  SLLTKLTPKEGISRVFAYNQMFSNLGQVIGPFIG----
                                                                                                                                  LGDRFGNHRLL-----LAALCYSFIMYFSSALAQTSFQLGVLRFAYGFGVGALMPSIN
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Pred. No. 8.6e-08;
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RESULT 12 AAE05852 ID AAE05

AAE05852 standard; Protein;

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Matches
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                                                                                                                                                                                                                                                                                                                                        The present sequence is a Pseudomonas stutzeri open reading frame-N (ORF-N) protein. The Pseudomonas stutzeri genome includes ORFs that encode enzymes required for biosynthesis of pyridine-2,6-bis (thiocarboxylate) (PDTC). The ORFs encoding PDTC are especially useful in environmental remediation methods, e.g. phytoremediation, bioaccumulation, water purification, waste water purification, solution mining mobilisation, immobilisation, detoxification, redox state modifier or modification of metal ion reactivity. In particular, the ORFs are useful for degrading carbon tetrachloride and removing metals from substrates, e.g. soil, or water.
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 32; Page 100-101; 172pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acids, useful for producing enzymes required to produce pyridine-2,6-bis (thiocarboxylate), especially useful for reducing the amount of metal or carbon tetrachloride in a substrate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JAN-2001; 2001WO-US02386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDTC; environmental remediation; phytoremediation; bloaccumulatic water purification; solution mining mobilisation; immobilisation; detoxification; redox state modifier; metal ion reactivity;
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                                VPVALVMAALVTYWVPAKSVSAP-
                                                         LALAFCFAGGVIAMISLRHVKTPGHMHNLTPREKFAELSRAVTLLYTNRNIFLSSI--VR
                                                                                     QSLANPATNQATAHSVPVARKAGVVGLKQSGVQASALLAGVALPPLVL-MWGWRGALAAW
                                                                                                                                                                                                     MGMPMMIFY----AIGILG
                                                                                                                                          GALVQRMGT--RAGLI-------CMFLLVGL---SFSLMAVLPGFGGLVTALLLCGTA 114
                                                                                                                                                                      SGVVAEIITPQKTMLIGFVLWCVFHVLFLVFGLGQANYGLILLFYGIRGLAYPLFLYSFI 127
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                                                                                                                                                                                                                                                          l Similarity
89; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD11172
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                                                                                                                                                                                                                                                                                                                    392 AA;
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                                                                                                                                                                                                                                                          Score 152.5; DB 7
Pred. No. 1.6e-07;
8; Mismatches 187
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                                                                                                                                                    for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by I
                                                                                                                                                                                                                                                                                                                                          The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, for heavetherical and bidges and the constalls his contribution.
                                                    monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chakraborty T, Domann E, Perez-Diaz J, Baquero F, Maduenio E, De Pablos B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,
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                                 .wipo.int/pub/published_pct_sequences
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bacterial infection; disease
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Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart
Soebel W, Kreft J, Kuhh M, Ng E, Vazquez-Boland JA;
nnal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A
Domann E, Hain T, Berche P, Charbit A, Durant L;
Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
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Best Local :
                                                                                                                                                        antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life
                                                                                                                                                                                                                                                                      ABN90538 to ABN93374 represent Staphylococcus epidermidis open reframe (ORF) nucleic acid sequences which encode the amino acid sequences in ABP35124 to ABP37960. The S. epidermidis sequences have
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                                                                      . epidermidis infection.
Jata for this patent did not form part of the printed
was obtained in electronic format directly from the
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Pred. No. 6.2e-07;
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                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum; brevibacterium lactofermentum; MCT; membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTLADKLGKKLIICIGLVF---FAVSEFMFAAGQ-SFTILIISRVLGGFSAGMVMPGVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQGFAGGLNSTFTSMGNFIGPLVAGALFDVNLEFPLYMATAVSLSGIIIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKGAAISVYNLSAGMSNFLAPAIAVVL----LPWFSTI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGLSAFETLFSLYTADKVNYTPKDISIAIIGGGVFGALFQVFFFDKFMKYMSELNFIAW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSLFGFAVIMPMMFVDELGFTTSE-WLQVWAAFFFTTIFSNIFWGIVAEKMGWMRVIRWF
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Pred. No. 9.9e-07;
76; Mismatches 190;
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109-JUL-1999

14-JUL-1999

14-JUL-1999

14-JUL-1999

27-AUG-1999

27-AUG-1999

27-AUG-1999

27-AUG-1999
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03-SEP-1999;
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31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
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27-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic lacids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.

AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum nucleic acids encoding and membrane transport proteins or their portions, identifying C. glutamicum or related bacteria, and transformation -
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N-PSDB; AAF67968.
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--NTLSLEGEAVIMPMMEVDELGETTSEWLQVWAAFFFTTIFS-NIFWGIVAEKMGWMRV
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                                                                                                                                                                                                                                                                                                                                                                                                           TMLIG-----FVLWCVFHVLFLVFGLGQANYGLILLFYGIRGLAYPLFLYSFIVV-
                                                                                                                                                                    GWLGKLIDILAIIATVFGTACSLGLGALQIGAGLSAANIIEDPSDWTIVGIVSVLTLAFI
                                                                                                                   KTPGHMHNLTPREKFAELS -- RAVTLLYTNRNIFLSSIVRII--
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99DE-1032230

99DE-103227

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99DE-1040831

99DE-1040831

99DE-104083

99DE-1041378

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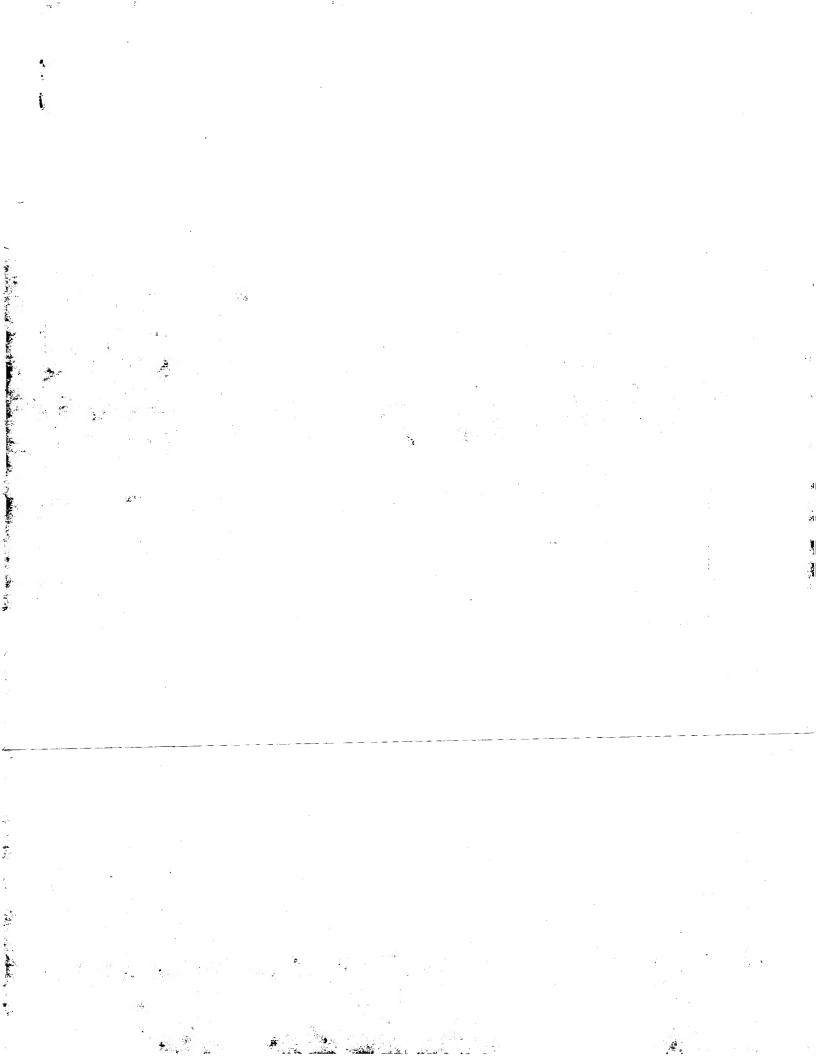
99DE-1041379

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                                                                       -FSAISGVGKGIQYL-SNANMVLAALLAIFVFVVGPTVSILNLLPGS
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20.5%;
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Pred. No. 1.9e-06;
0; Mismatches 154
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	Search completed: March 13, 2003, 16:53:13 Job time : 36.7483 secs	r r .
	Db 453 LSGGDNALSNLQNVTIVAATPELEVVIGLMEA 484	_
	QY 362 SAGMSNELAPAIAVVLLPW-FSTIGVVIA 389	_
452	Db 393 PGGQIMGIIAMILLGTEFITSADSASTVMGTMSQHGQLEANKWVTAAWGVATAAIGLTLL 452	_
361	Qy 322KGAAISVYNL 361	_
392	Db 339 REFILGVLLVPAGVSTVWFSIFG GTAIVF EQNGESIWGDGAAEEQLFGLLHAL 392	_
321	Oy 294 IR	_
338	Db 282 IGNYLSNFFQMAGRTAMSADGTAGEWLGSWTIFYWAWWISNSPFVGMFLARISRGRS 338	п



Run on:

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Minimum DB seq length: 0
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Perfect score:
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    Maximum Match 100%
Listing first 45 summaries
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US-09-134-001C-3020
US-09-333-254-2
US-09-333-254-2
US-09-183-270-2
US-09-184-001C-5594
US-09-134-001C-5210
US-09-134-001C-3487
US-09-134-001C-3487
US-09-134-001C-4435
US-09-134-001C-5370
US-09-134-001C-5370
US-09-134-001C-5370
US-09-134-001C-5370
US-09-134-001C-3949
US-09-031-392-4
US-09-031-392-4
US-09-134-001C-3433
US-09-134-001C-3433
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US-09-134-001C-3431
US-09-134-001C-3431
US-09-134-001C-3431
US-09-134-001C-3912
US-09-134-001C-3912
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Patent No. 6380370

PATENT INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC 07

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

PRIOR FILING DATE: 1997-08-14
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SEQ ID NO 3020
LENGTH: 467
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Result

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Sequence 10, Appl	Sequence 10, Appl	Sequence 4353, Ap	Sequence 3743, Ap	Sequence 2, Appli	Sequence 15, Appl	Sequence 3355, Ap	Sequence 5557, Ap	Sequence 4130, Ap	Sequence 5365, Ap	Sequence 4074, Ap	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 5, Appli

ALIGNMENTS

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STAPHYLOCOCC

Query Match Best Local Similarity 48.6%; Pred. No. 6.5e-96; Matches 195; Conservative 76; Mismatches 129; Indels 1; Gaps Qy 10 GLPLHLIWGYIĀLAVEMTGDGEELAFLSHYIKSLGFPARASFAFTLYGLAAALSAWVS 69 Qy 10 GLPLHLIWGYYĀLAVEMTGDGEELAFLSHYIKSLGFPARASFAFTLYGLAAALSAWVS 69	EYYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAVFPALEPKHKGAAISVYNLSAGMSNE 368
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Query Match 47.1%; Score 1040.5 Best Local Similarity 48.6%; Pred. No. 6. Matches 195; Conservative 76; Mismatche	AEASFAFTLYGLAAALSAWV. : : : : : TQATLLFTVYGFLAAISSWG
	DB 4; Length 467; 2-96; 129; Indels 1; Gaps

Length 416; Indels

77;

Gaps

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TYPE: PRT
; ORGANIZM: Pseudomonas mendocina KR-1
US-09-333-208-2
                                                                                                                                                                                                                          Sequence 2, Application US/09333254A Patent No. 6235882
                                                                                                                                                                                                       GENERAL INFORMATION:
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SOFTWARE: Microsoft Office
SEQ ID NO 2
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                                APPLICANT: Chen, Kevin K.

TITLE OF INVENTION: A Gene Encoding a Putative Efflux Protein
TITLE OF INVENTION: Antiblotics in Pseudomonas Mendocina
FILE REFERENCE: CL-1160-D
CURRENT APPLICATION NUMBER: US/09/333,254A
CURRENT FILING DATE: 1999-06-15
EARLIER APPLICATION NUMBER: 08/961,738
EARLIER APPLICATION NUMBER: 08/961,738
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Best Local 9
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                      NUMBER OF SEQ ID NOS
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; TYPE: PRT
; ORGANISM: Pseudomonas mendocina KR-1
US-09-183-270-2
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Best Local S
Matches 88
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SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Microsoft
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 6
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TYPE: PRT
ORGANISM: Pseudomonas mendocina KR-1
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                                                                                64 SAWVSGVVAEIITPQ---KTMLIGEVLWCVFHVLFLVFGLGQANYGLILLFYGIRGLAYP 120
                                                                                                                       66 VAVVVLLTGLVAATYGFGIYLFAQLVPDM---QASLGFGFSYVGTITASAQLGFLLCAML 122
                                                                                                                                                              20 IAIAVEMTG-----DGFELAFLSHYIKSLGFTPAEASFAFTLYG------LAAAL 63
                                                                                                                                                                                                                       Local Similarity
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                                         AVW------LTPKVGGGRMIAASGAVCALALLLIPLSSNTFVIGVLLTL--LAGTAAT 172
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Pred. No. 9.8e-08;
B; Mismatches 164
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Indels Length

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US-09-134-001C-5594
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LENGTH: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
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                                                                   ---SLLYSAIVLVML--VLANGYWTIMIISFVV-----FIGFDMIRPALTNYFSNIAGK
                                                                                                                                                                                      LSLFGFAVIMPMMFVDELGFTTSE-WLQVWAAFFFTTIFSNIFWGIVAEKMGWMRVIRWF
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                                                                                                        GCLGMAASSLAFYYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAVFPAL-----EPK
                                                                                                                                              FGLSAFETLFSLYTADKVNYTPKDISIAIIGGGVFGALFQVFFFDKFMKYMSELNFIAW-
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19.7%; Pre
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Pred. No. 2e-06;
6; Mismatches 1
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US-09-134-001C-4847
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                                                                                                                       Sequence 5210, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
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LENGTH: 492
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNO EILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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Local Similarity 20.2%;
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Pred. No. 2.2e-05;
                                                                 AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC FOR DIAGNOSTICS AND THERAPEUTICS
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RESULT 8
US-09-134-001C-3564
Sequence 3564, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5210
                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3564
LENGTH: 473
                                                                                                                          Query Match
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Best Local
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
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  30 LSVORKLWLRNFMOAFFVVFFVYMAMYLIRNNFKAAQPLLK---EEIGLTTLELGYIGLA
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                                                                                                     Local Similarity
                                          1 MSRNNKQWLG--LPLHLIWGYIAIAVFMTGDGFELA--FLSHYIKSLGFTPAEASF---A 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKMSPETQLFGVFNHIPLGIVLSIIALLLIASLLCYF 422
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                                                                                Score 126.5; DB 4;
Pred. No. 0.00019;
3; Mismatches 169;
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Pred. No. 4e-05;
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LENGTH: 477
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                      Matches
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TITLE OF INVENTION: NUCLEIC, ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
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  LGWYWAVYSV-GIGV--
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                                            LTGLFVDLF --
                                                                              LWCVFHVLFLVFGLGQANYGLILLFYGIRGLAYPLFLYSFIVVIIHNVRSENSSS----A
                                                                                                                                                                FLSHYIKSLG---FTPAEASFAFTLY----GLAAALSAWVSGVVAEIITPOKTMLIGFV
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                                                                                                                                                                                                                                                                                                         Similarity
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22.2%;
                                          ---SWRMPFYLVSAIAAVAFILGFFFV-----
AGSYIPSFTIPIMGEMGTLWLALAFCFAGGVIAMISLRHVKT 198
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                                                                                                                                                                                                                                                                           7%; Score 125; DB 4;
2%; Pred. No. 0.00027;
174; Mismatches 172;
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Length 477; Indels

Gaps 34

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ENNTKTKDIV 203

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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4435

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GENERAL INFORMATION:
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SEQ ID NO 4435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4435, Application US/09134001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                       AFFF--TTIFSNIFWGIVAEKM--GWMRVIRWFGCLGMAASSLAFYYMPQYFGHNYWMAM
                                                                            TTKEILFKYVLN-----NKWVWAIAFTNIFVYFVRYGVLDWAPTYLSEEKHFDLSASGWA
                                                                                                                                                                                                                                          GFSV----SERGSKTSIWNVA-HNVGGG
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                                                                                                                                                                                                                                                                                                                                             EIITPQKTMLIGFVLMCVFHVL--FLVFGLGQANYGLILLFY--GIRGLAYP----LFLY 124
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YFLYEWAGIPGTLLCGYLSDKLFKGRRGPAGFFFMLGVTIFILIYWLNPP--GH-AWLDN 386
                                                                                                                     TURNIFLSSIVRIINTLSLFGFAVIMPMMFVDELGFTTSEWLQV--
                                                                                                                                                          FGYLKGFEGVFIYPALLAIIIAIFSYILIRDTPQSQGLPPIEQYKNDYATSTKQTIETEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                          5.6%; SCULT 19.5%; Pred. NO. U.UUUT 19.5%; Pred. NO. U.UUUT 190;
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                                                     IF----SNIFWGIVAEKMGWMRVIRWF-GCLGMAASSLAFYYMPQYFGHNYWMAMIP---
                                                                                                                                       SRAVTLLYTNRNIFLSSIVRIINTLSLFGFAVIMPMMFVDELGFTTSEWLQVWAAFFFTT
                      ISYLIGTNIF-GILAHKMG----
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RESULT 11
US-08-063-552-4
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                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKÉT NUMBER: 9067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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CORRESPONDENCE ADDRESS:
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                                                                                                                      111 FYGIRGLAYPLFLYSFIVVIIHNVRSENSSSALGWYWAVYS-----VGIGVAGSYI- 161
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233 VLVGPPFGSVLYEFVGKTAPFLVLAALVLLDGAIQLFVLQPSRVQPESQKGTP------
                                                                                                                                                           133 GLLFASKATVQLLTNPFIGLLTNRIGYPIPMFAGF---CIMFISTVMFAF-SSSYAFLLI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 19930: CLASSIFICATION: 53
                                                                                                                                                                                                58 GLAAALSAWVS------GVVAEIITPQKTMLIGFVLWCVFHVLFLVFGLGQANYGLILL 110
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                   ----PSF---TIPIMGEMGTLWLALAFCFAGGVIAMISLRHVKTPGHMHNLTPREKFAEL
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                                                                              -SSCSSVAGMGMLASVYTDDEERGKPMGIALGGLAMG
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                                                                                                                                                                                                                                                                               Score 123.5;
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PCT-US93-05704-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (818) 795-6321 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:

NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 515 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: PCT/US93/05704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 FYGIRGLAYPLFLYSFIVVIIHNVRSENSSSALGWYWAVYS------VGIGVAGSYI- 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 GLAAALSAWVS-----GVVAEIITPQKTMLIGFVLWCVFHVLFLVFGLGQANYGLILL 110
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CITY: Pasadena
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-AIALGTFVAAFVPMAAVFPALEPKHKGAAISVY---NLSAGMSNFLAP----AIAVVL-
                                                                                                                                      IF----SNIFWGIVAEKMGWMRVIRWF-GCLGMAASSLAFYYMPQYFGHNYWMAMIP---
                                                                                                                                                                                                     --LTTLLKDPYILIAAGSICFAN----MGIAMLEPALPIWMMETMCSRKWQLGVAFLPAS
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3; Mismatches 157;
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TELEFAX: 919 881 3175 INFORMATION FOR SEQ ID NO: 5:
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TITLE OF INVENTION: OX
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS
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ATTORNEY/AGENT INFORMATION:
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                                        179 LI-----MGILIILIAFV-;------IRFPG---
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223 THRNIFLSSIVRIINTLSLEGEAVIMPMMEVDELGETTSEWLOVWAAFE---
                                                                                                                          134 WFPDKRGLASGFTAAGYGLGVLPFLPLISSVLKVE--
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                                                                                                                                                                                                          77 VDKFGPRIPLMFGGAMVLAGWTFMGMVDSVPALYALYTLAGAGVGIV---YGIAMNTANR 133
                                                                                                                                                                                                                                                 72 AEIITPOKTMLIGFVL----WCVFHV-----LFLVFGLGQANYGLILLFYGI-----
                                                                                                                                                                                                                                                                                          17 WFYLVLAVILIMCMISGVQYSWTLYANPVKDNLGVSLAAVQTAFTLSQVIQAGSQPGGGYF 76
                                                                                                                                                                                                                                                                                                                                 17 WGYIAIAVFM----TGDGFELAFLSHYIK-SLGFTPAEASFAFTLYGLAAALSAWVSGVV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 57
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                             SFTIPIMGEMGTLWLALAFCFÄGGVIAMISLRHVKTPGHMHNLTPREKFAELSRAVTLLY
                                                                                                                                                               -----RGLA-----YPLFLYSFIVVIIHNVRSENSSSALGWYWAVYSVGIGVAGSYIP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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US-09-134-001C-5370
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
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SEQ ID NO 5370
LENGTH: 499
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                                    393 LYLLAFVLCAF 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 -----VSGGAFAFSFLSFGRYVSFFSSWFLTFGYVCVVALNATAFSLLIKFLLPNV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 WG----AFILPGD------WIKQSG--PIASSIGIVIGALLMILIAVSYGALVEKFP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IHNVRSENSSSALGWYWAVYSVGIGVAGSYIPSF-TIPIMGEMGTLWLALAFCFAGGVIA 189
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TCLSATKLFSF
                                                                                                                                                          L-----NGNLWLTGAVTQDAFGFIGLAVLAVAIIMGIFTGLNGFLMSSSRLLFSMG
                                                                                                                                                                                                  LAFYYMPQYFGHNYWM-----
                                                                                                                                                                                                                                                                                 PMMFV--DELGFTTSEWLQVWAAFFFTTIFSNIFWGIVAEKMGWMRVIRWFGCLGMAASS
                                                                                                                                                                                                                                                                                                                                                MISLRHVKTPGHMH-NLTPREKFAELSRAVTLLYTNRNIFLSSIVRIINTLSLFGFAVIM 248
                                                                                                                                                                                                                                                                                                                                                                                                          LNNGKLYTVAG-----WDVYITEIVIATVLLIVFMLITIRGASVSGSLQYYFCVA--MVL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQKTMLIGFVLWCVFHVLFLVFGLGQANYGLILLFYG-----IRGLAYPLFLYSFIVVI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LSAGMSNF---LAPAIAVVLLPWFSTIGVVIAYTALYLLAFVLCAFI--RVEQP
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                                                                              RSGIMPTVFSKLHSKHKTPYVAIIFLVA--VSLIAPWLGRTALTWIVDMSSTGVSIAYFI
                                                                                                                  ----MAAVFPALEPKHKGAAISVYNLSAGMSNFLAPAIAVVLLPW----FSTIGVVIAYTA 392
                                                                                                                                                                                                                                           PWAYVGFDNIPQTAEEF-----NFSPNKTFKLIVYSLLAASLTYVVMLLYTGWLSTQATS
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Pred. No. 0.00057;
50: Mismatches 169;
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US-09-134-001C-3949
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Search completed: March 13, Job time: 13.5828 secs
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Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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SEQ ID NO 3949
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Best Local (
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CURRENT APPLICATION NÜMBER: US/09/134,001C
CURRENT FILING DATE: |1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 VYSVGIGVAGSYIPSFTIPIMGEMGTLWLALAFCFAGGVIAMISLRHVKTPGHMHNLTPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 FHVLFLVFGLGQANYGLILLFYGIR-GLAY-PLFLYSFIVVIIHNVRSENSSSALGWYWA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 YILSYINFLPTVTSİAIAITSFAFSIHFIADAATNFVIGFLLKKFGSKLVLTSGFLL--A 104
                                                                                                                                                                                                       G----HNYWMAMIPAIALGTFVAAFVPMAAVFPA--LEPKHKGAAISVYNLSAGMSNFLA
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                                                                                                                     PAIAVVLLPWFSTIGVVIAYTALYLLAFVL 400
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                                                                               PLVGGLITQFTNNLNNTFYFSAMIFLALAV
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Maximum DB seq length: 2000000000
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Perfect score:
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
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      US-09-802-208B-5
2211
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Listing first 45 summaries
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    В
      US-09-802-208B-5
US-09-738-626-6943
US-09-738-626-6943
US-10-122-466A-11
US-09-815-242-10467
US-09-815-242-10467
US-09-738-626-6196
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US-09-738-626-3974
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Sequence 52, Appli
Sequence 3627, App
Sequence 11, Appl
Sequence 11592, Ap
Sequence 10592, Ap
Sequence 6555, Ap
Sequence 6729, Ap
Sequence 6196, Appl
Sequence 4815, Appl
Sequence 10, Appl
Sequence 11180, A
Sequence 11180, A
Sequence 29, Appl
Sequence 520, Appl
Sequence 5100, Appl
Sequence 5100, Appl
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LILLFYGIRG PIMGEMGTLW	ength 424; ndels 0; Gaps PAEASFAFTLYGLA 60 PAEASFAFTLYGLA 60 LILLFYGIRGLAYP 12	Selectable Markers		Sequence 385, App Sequence 2, Appli Sequence 431, App Sequence 431, App Sequence 475, Appli Sequence 572, Appli Sequence 5733, App Sequence 5712, App Sequence 5712, App Sequence 5714, Ap Sequence 5741, Ap Sequence 5741, Ap Sequence 11824, Ap Sequence 1784, Ap Sequence 274, Appli Sequence 274, Appli Sequence 274, Appli Sequence 106, Appli Sequence 11912, Ap Sequence 106, Appli Sequence 11912, Ap Sequence 11912, Ap Sequence 3844, Ap Sequence 5744, Ap Sequence 5744, Appli Sequence 4875, Appli Sequence 38, Appli Sequence 5144, Ap Sequence 5144, Ap Sequence 5144, Ap Sequence 38, Appli Sequence 51610, Appli Sequence 51610, Appli Sequence 51610, Appli Sequence 6110155, Appli Sequence 6110155, Appli Sequence 6110155, Appli Sequence 6110155, Appli Sequence 6110155, Appli Sequence 6110155, Appli Sequence 6110155, Appli Sequence 6110, Appli Sequence 61101555

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US-09-738-626-3627
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US-09-738-626-3627
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
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                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                         VVIIHNVRSENSŚSALGWYWAVYSVGIGVAGSYIPSFTIPIMG--EMGTLWLALAFCFAG 185
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                                                       VIMPMMFVDELGFTTSEWLQVWAAFFFTTIFS----NIFWGIVAEKMGWMRVIRWFGCL 300
                                                                                    SLIALLGVKE-RRGRHPLVANPDDVKQTLGQGFKLLRNDRRARFVTYIRTINSIPTYAMA
                                                                                                              GVIAMISLRHVKTPGHMHNLTPREKFAELSRAVTLLYTNRNIFLSSIVRIINTLSLFGFA 245
                                                                                                                                                                                                AAALSDLWGPRKVMILGASIWIVFELIFLTVALTTDHTWLIFLAYGLRGFGYPFFAYGFL 131
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TATEISHI, NAOKO
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89; Mismatches 188
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; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6943 i
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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Best Local Similarity
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                                               237 -- NTLSLEGFAVIMPMMEVDELGETTSEWLQVWAAFFFTTIES-NIEWGIVAEKMGWMRV 293
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IGNYLSNFFQMAGRTAMSADG;---TAGEWLGSWTIFYWAWWISWSPFVGMFLARISRGRS
                                                                                                                                                     KTPGHMHNLTPREKFAELS----RAVTLLYTNRNIFLSSIVRII---
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Pred. No. 0.00014;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MUTANT LACTIC BACTERIA WITH A CAPACITY TITLE OF INVENTION: OVEREXPRESSING AT LEAST ONE PEPTIDASE FILE REFERENCE: 1096-02
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TYPE: PRT
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                    GVVIAYTALYLLAF
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DELORME, CHRISTINE
RENAULT, PIERRE
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SEQ ID NO 10592
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
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Yamamoto, Robert T.
Xu, H. Howard
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Zyskind, Judith W.
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                  -PALEP-----KHK----GAAISVYNLSAGMS 366
139; DB 10;
No. 0.00023;
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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TATEISHI, NAOKO
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OCHIAI, KEIKO
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                                                                                                                                                                                                                                                                                  ·----FAMSFVVGIVGMGIMRLLKKPEYL----DRDTVNSVSGAAT-----
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                                                                                                                    -----FWVAPRFFGEKWLERAI--FGWGWATAAVATGIALL
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US-09-815-242-10467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-09-815-242-10467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 10467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
DELICA ETITMC DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER:
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  364
                                       314 FLCPLFFISVKNSSLIGLCLFGLMFTNLGIAGLVP-KFIYDYFPTKLRGLGTGLIYNLGA
                                                                             310 YYMPQYFGHNYWMAMIPAIALGTF----VAAFVPMAAVFPALEPKHKGAAIS-VYNLSA
                                                                                                                      276 LMTIAGLG-----
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                                                                                                                                                                                                                                                                                  186 YGWRNSFFIGLLPVLLVLWI--
                                                                                                                                                                                                                                                                                                                                                                                                       121 LFLYSFIVVI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 SAWVSGVVAEIITPQKTMLIGFYLWCVFHVLFLVFGLGQANYGLILLFYGIRGLA---YP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 WLGLPLHLIWGYIAIAVFMTGDGFE---LAFLSHYIKS-LGFTPAEASFAFTLYGLAAAL 63
                                                                                                                                                          MMFVDELGFTTSEWLQVWAAFFFTTIFSNIFWGIVAEKMGWMRVIRWFGCLGMAASSLAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGFFGAMADKY-GRKPMM---:MWAIF-----IYSVGT-----GLSGIATNLYM 125
--GMSNFLAPAIAVVLLPWF - - - STIGVVIAYTALYLL
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20.3%; | Pred
20.3%; | 69;
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                                                                                                                      -TLTGTIFFGFVGDKIGVKKAF----VVGLITSFI--
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9; Mismatches 136;
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Indels 161; Length 425;

Gaps

23;

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162

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313

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373 TGGMA---APVLATYISGYYGLGVSLFIVTVAFSALLIL 408

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RESULT 9
US-09-738-626-6196
; Sequence 6196, Application US/09738626
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US-09-738-626-6729, Application US/09738626; Publication No. US20020197605A1
GENERAL INFORMATION:
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US-09-738-626-6729
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Best Local Similarity 22.4
Watches 93; Conservative
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SEQ ID NO 6729
LENGTH: 378
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OZAKI, AKIO
TITLE DEFENENTION: NOVEL POLYNUCLEOTIDES
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                                                                                                                                                                                                                                                      304 ASSLAFYYMPQYFG-HNYWMAMIPAIALGTFVAAFVPM----AAVFPALEPKHKGAAISV 358
                                                                                                                                                              359 Y------NLSAGMSNFLAPAIAVVLLPWFSTIGVVIAYTALYLLAFVLCAFIRV 406
                                                                                                                                                                                                                                                                                                                                              246 VIMPMMFVDELGFTTSEWLQVWAAF--FFTTIFSNIFWGIVAEKMGWMRVIRWFGCLGMA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 LGWYWAVYSVGIGVAGSYIPSFTIPIM----GEMGTLWLALAFCFAGGVIAM-----
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                                                                                                                                                                                                          SMAL----MGINNLWVTL---VALFVFTAAFFALHSSASGWIGIIATKDRAEASSM
                                                                                                                                                                                                                                                                                                  MI-----DQFGL--SEVL-VGAVFIMYLAGTWSSTQAGALREKIGNGSTVIFLSLTMIA 275
                                                                                                                                                                                                                                                                                                                                                                                          FQPKNINLRHEISAMAAHWRNPR------LALLFGTAFLGMGTFVSLYNYL---GFR 224
                                                                                                                                                                                                                                                                                                                                                                                                                                      ----ISLRHVKTPGHMHNLTPREKFAELSRAVTLLYTNRNIFLSSIVRIINTLSLFGFA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGIYIAGNTVG-GLTGRMIPAGLLEVTHWQNALLGSSIAALIF----GVIMVVLLPKQRK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLPTMTEELGITPTESALTVSATTGMLALCIVPASILSEKFGRGRVLTISLTLAIIVGL 76
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OCHIAI, KEIKO
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ANDO, SEIKO
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GENERAL INFORMATION

APPLICANT: NAKAGAWA, SATOSHI

HIROSHI

APPLICANT:

APPLICANT:

HAYASHI, MIKIRO OCHIAI, KEIKO MIZOGUCHI, H ANDO, SEIKO

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RESULT 10
US-09-738-626-6877
; Sequence 6877, Application US/09738626
; Publication No. US20020197605A1
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SEQ ID NO 6196
LENGTH: 701
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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                                                                                                                                                                                350 -- KHKGAAISVYNLSAGMSNFLAPAIAVVLLPWFSTIGVVIAYTALYL 395
                                                                                                                                                                                                                                                                                                                                                              261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 TYAVIGMAISGVVNALLRMDFSDLFTTNYGLLVFAKAVGVVVVGMFGLAH-----RTFTI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 AGGDHDYGTNSLLWHLVLMLLWVGGL------MALIAHARRIGPNMDMAVKRYSIIA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 --GQANYG------LILLFYGIRGLAYPLFLYSFIVVIIHNVR-SENSSSALGWY--WA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 AIAFEQVALAKAW-AWVAGFAFITGIAGLFC--RTWLAQPLLFAGSIIMTVPLGLEGHSA 210
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                                                                                                                                    PGLHEWAAVMTDN-----PLLKFIMHPAVNTIQFIIIFYALYL 525
                                                                                                                                                                                                                                                                       FGC--LGMAASSLAFYYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAVFPALEP----
                                                                                                                                                                                                                                                                                                                   LEMGYSLEKEPTLLNVFTMWRFDLMLGTIGIMLLAFYMYGLVALRRQAKKWNHMRTFWWV
                                                                                                                                                                                                                                                                                                                                                                                                          PKLEKDPKNSALFTRI------AIVEVLAMAAVTGVAISMGRTPPPAPEIQDLSVMA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYSV-GIGVAGSYIPSFTIPIMGEMGTLWLALAFCFAGG--VIAMISLRHVKTPGHMHNL 205
                                                                                                                                                                                                                                                                                                                                                              SEW------AEKMGWMRVIRW-
                                                                                                                                                                                                                            LGCITLVVTVSSGIGMNMPATFSMHMVAHMLLSMVVPVFLVLGAPLSLIMEAVAPGEPGR 487
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91; Conserv
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SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.9%; Score 130; DB 9; 22.3%; Pred. No. 0.0024;
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                                                                                                                                          Sequence 4815, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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                APPLICANT:
                                                APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSH
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, HAYASHI, MIXIRO
APPLICANT: OCHIAI, KEIKO
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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CURRENT FILING DATE: 2000-12-18
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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Local Similarity 21.3%;
ses 97; Conservative 7
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                                                                                                                                                                                                                                                                                                                                        IIWVYFLFTIAELLLSPVGNSLATKVAPEAFQSRMFAVWL-----MAVSMGTSLSGTLGG
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                       MIZOGUCHI, HIROSHI
ANDO, SEIKO
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US-09-922-501-10
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LENGTH: 450
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APPLICANT: Dartois, Veronique A.
APPLICANT: Hoch, James A.
APPLICANT: Valle, Fernando
APPLICANT: Kumar, Manoj
TITLE OF INVENTION: 2, 5-DKG¹PERMEASES
FILE REFERENCE: P-SR 4877
CURRENT APPLICATION NUMBER: US/09/922,501
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 09/633,294
PRIOR APPLICATION NUMBER: US 09/677,032
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 TILAAVLSFLFLKDVPVTANFRQQIDIFGNKNTWILSIIYLMTFGAFAGFAAQFGLIINN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 -FTIPIMGEMGTLWLALAFCFAG------GVIAMISLRHVK-TPGHMHN----LTPR
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llarity 21.2%; Pred. No. 0.0022;
Conservative 62; Mismatches 163;
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; ORGANISM: Pantoea
US-09-922-501-10
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            CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                Sequence 11180, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows
SEQ ID NO 10
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                                                                                                                                                                                         TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 LNGLTGGPGASYTFMAIALLVSVGLVFFLKV 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 VRVGWLA--AVPYLAAIITMLVISWLSDKTGLRRLFIWPLLL---IASVTFFGSWLLGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 LASAMAEEQQAIPPMRNVPQALRSRNVVVLCLLHALWSIGVYGFMMWMPSILRSAASMDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 ----FAELSRAVTLL-----YTNRNIFLSSIVRIINTLSLFGFAVIMPMMF--VDELGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 TVLWMSIVSGYLINAFGWREMFIFE-GVPALIWAIFWWFIVR--DKPEQVSWLTETEKQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 T-LWLALA------FCFAGGVIAMI-----SLRHVKTPGHMHNLTPREK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 SNIPA------LMVIRFVLGVVEAAVMPAMLIYISNWFTRQERSRANTFLVLGNPV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 HNVRSENSSSALGWYWAVYSVGIGVAGS-----YIPSF-----TIPIMGEMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 SRGTSSLIG----ALFFLGYFIFQVPGAIYA---VKRSVRKLVFTSLLLWGFCAAATGLI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 TPQKTMLIGFVLWCVFHVLFLVFGLGQANYGLILLFYGIRGLAY-PLFLYSFIVV---II 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 WWYLMPVIFIT---YSLAYLDR------ANYGFAAA-----SGIEADLGI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 WGYIAIAVFMTGDGFELAFLSHYIKSLGFTPAEASFAFTLYGLAAALSAWVSGVVAEI-I 75
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                                                                                                                                                                                                                                                                                                                          Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                            Carr, Grant J.
Yamamoto, Robert T
                                                                                                                                                                                                                                                                                                               Wall, Daniel
                                                                                                                                                                                                                                                                                             Trawick, John D.
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20.8%;
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Pred. No. 0.003;
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR ETLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS::14110
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 11180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-738-626-6795
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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Best Local Similarity 20.8
94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6795, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 V------VGSVVLAYSFQTAIALLAII 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 LLTPLLLPHIGWRGMFLVGIFPAFVAWFLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 YIPSFTIPIMGEMGTLWLALAFCFAGGVIAMISLRHVKTPGHMHN------LTPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 GL------AYPLFLYSFIVVIIHNVRSENSSSALGWYWAVYSVGIGVAG-S 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 GAVFGGILFGALSD-----KYGRVRVLTWTI--LLFAVFTGLCAIAQ-GYWDLLIYRTIA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 AAALSAWVSGVVAEIITPQKTMLIGFVLWCVFHVLFLVF----GLGQANYGLILLFYGIR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 NSYGWKAL-----IGSAVGYGMDGFDLLILGFMLSAISADLNLTPAQGGSLVTWTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 NNKQWLGLPLHLIWGYIAIAVFMTGDGFELAFLSHYIKS----LGFTPAEASFAFTLYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAVVLLPWFSTIG-VVIAY---TALYLLAFV 399
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                                                                                                                                                                                                                                                                        HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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RESULT 15
US-10-024-623-29
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US-10-024-623-29
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6795
                                                                                     SEQ ID NO 29
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Best Local :
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PRIOR APPLICATION NUMBER: US 60/256,240
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/256,588
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/258,028
PRIOR APPLICATION NUMBER: US 60/258,028
PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/024,623 CURRENT FILING DATE: 2001-12-17
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181, TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF TITLE OF INVENTION: USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Curtis, Rory A.J
                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                             NUMBER OF SEQ ID NOS:
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                                         LENGTH: 47
TYPE: PRT
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TYPE: PRT
                   ORGANISM: Escherichia coli
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394 DFGITCSTTTNWVSNMIIGATFLTLLDSIGAAGTFWLYTALN-IAFVGITF 443
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                            GAATSVYNLSAGMSNELAPATAVVLLPWESTIGVVIAYTALYLLAEVLCAE
                                                               {\tt MALGTLVLGYCLMQFDNGTASSGLSWLSVGMTMMCIAGYAMSAAPVVWILCSEIQPLKCR}
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                                                                                               MAASSLAFYYMPQYFGHN----YWMAM-IPAIALGTFVAAFVPMAAVF-PALEP-KHK
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73; Mismatches 163;
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Search completed: March 13, 2003, 16:51:26 Job time: 14.9338 secs

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N;Alternate names: ribicol transporter
C;Species: Klebsiella pneumoniae
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 08-Oct-1999
C;Accession: S78599
R;Heuel, H.: Turgut, S.; Schmid, K.; Lengeler, J.W.
J. Bacteriol. 179, 6014-6019, 1997
A;Title: Substrate recognition domains as revealed by active hybrids between the D-ar A;Reference number: S78599; MUID:97464425; PMID:9324246
A;Accession: S78599
A;Molecule type: DNA
A;Residues: 1-427 <HEUD
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TEKA 420
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R.Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Masuda, S.; Maueel A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Althors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A.; Maccession: H69607
A.; Status: preliminary: nucleic acid sequence not shown: translation not shown
A. McCession: Prop. Numa
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C;Date: 05-Dec-1997 #
C;Accession: H69607
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C;Superfamily: hypothetical protein c0103
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conserved hypothetical protein
C; Species: Bacillus subtilis
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#sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
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R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.; (; Lory, S.; Olson; M.V. Nature 406, 959-964, 2000
A;Title: Complete genome sequence (A;Reference number: A82950; MUID: 20
                                                                                                                                                                                            C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision
                                                                                                                                                                                                                             probable MFS transporter PA4233 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa
                                                                                                                                                                     C; Accession: D83117
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R;Kunst, F.; Ogasawara, N.; Moszer, T.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber R;Kunst, F.; Ogasawara, N.; Moszer, T.; Entian, K.D.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmersch, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997 |

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddle, Y.; Sato, T.; Scanlard, A; Winthors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A;Reference number: A69580; MUID:98044033; PMID:9384377

A:Status, orellminary: nucleic acid sequence not shown translation not shown
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C;Superfamily:
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A;Experimental source: strain 168
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C;Accession: D69895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 GVCLEAFGAKRTMFMGLLFYVIGTAAFIVFGFEQLNLPVMYVTYFVKGLGYPLFAYSFLT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 LGLPLHLIWGYIAIAVFMTGDGFELAFLSHYIKSLGFTPAEASFAFTLYGLAAALSAWVS
FVGPALAWLFIGLVGAQGVVWIFAALYLASAVLTKCIHIPE-----
                                                      FLAPAIAVVLLPWFSTIGVVIAYTALYLLAFVLCAFIRVEQPGFSSAPVTEKAL 421
                                                                                                                                                                                                 AFYYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAVFPALEPKHKGAAISVYNLSAGMSN
                                                                                                                                                                                                                                                              LPMHMAQH-GISTNVWLQIWGTIFLGNIVENLIFGIVGDKEGWKNTVIWFGGVGCGIFTV
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                                                                                                                                       LLYYAPVFSGGSLAVVSVIGFIWGGLLAGYVPIGAIVPTVAGKDKGAAMSVLNLAAGLSA
                                                                                                                                                                                                                                                                                                                                     MPMMFVDELGFTTSEWLQVWAAFFFTTIFSNIFWGIVAEKMGWMRVIRWFGCLGMAASSL
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139; Conserv
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33,68; Pred. No. 2.8e-45;
tive 88; Mismatches 172;
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quence of Pseudomonas MUID:20437337; PMID:1

omonas aeruginosa PMID:10984043

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opportunistic

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Coulter, S.N.; Folger, I 15-Sep-2000

; Warrener,
K.R.; Kas,

Hickey, Larbig,

Χ.

#text_change 31-Dec-2000

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A;Accession: D83117
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-462 <STO>
A;Cross-references: GB:AE004840,
A;Experimental source: strain P)
C;Genetics:
A;Gene: PA4233
C;Superfamily: Escherichia coli
                                                                                                                                                       A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-456 <ARN>
A;Residues: 1-456 <ARN>
A;Cross-references: GB:AE001325; GB:AE001273; NID:g3328980; PIDN:AAC68146.1; PID:g332898
A;Cross-references: GB:AE001325; GB:AE001273; NID:g3328980; PIDN:AAC68146.1; PID:g3328980;
A;Cross-references: GB:AE001325; GB:AE001273; NID:g3328980; PIDN:AAC68146.1; PID:g3328980;
                                                                                                                                                                                                                                                                                                                                                      probable hexosphosphate transport - Chlamydia trachomatis (serotype D, strain C;Species: Chlamydia trachomatis C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999 C;Accession: A71501
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                                                                                                                      A; Experimental source: serotype C; Genetics: A; Gene: uhpc C; Superfamily: hexose phosphate
                                                                                                                                                                                                                                                               A;Title: Genome sequence of an obligate intracellular pathogen A;Reference number: A71570; MUID:99000809; PMID:9784136 A;Accession: A71501
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Residues: 1-462 <STO>
:Cross-references: GB:AE004840; GB:AE004091; NID:g9950442; PIDN:AAG07621.1; GSPDB:GN00:
                                                                   Query Match
Best Local Similarity
                                                                                                                    Superfamily: hexose phosphate transport protein uhpT
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                1 MSRNNKQW-LGLPLHLIWGYIAIAVFMTGDGFELAFLSHYIKSLGFTPAEAS-FAFTLYG
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                                                 Score 180.5; DB 2;
Pred. No. 4.3e-06;
1; Mismatches 171;
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                                                   Indels 123;
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RESULT
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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene:
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A; Residues: 1-456 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AL590842; PIDN:CAC92404.1; PID:g15981107; GSPDB:GN00175
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Local Similarity 22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                        1 MSRNNKQWLGLPLHLIWGY-IAIAVFMTGDGFELAFLSHYIKSL-GFTPAEASFAFTLYG
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                                                   GLQALFWGIAILALLGIVITLTVVPSANSHVLNRESSMVKGSVSKVLHNSRLLKLNFGIM
                                                                                                                                                                                                     YPLFLYSFIVVIIHNV-RSENSSSALGWYWAVYSVGIGVAGSYIPSFTIPIMGEMGTLWL
                                                                                                                                                                                                                                                                                                            LAAALSAWVSGVVAEIITPQKTMLIGFVLWCVFHVLFLVFGLGQANYGLILLFYGIRGLA 118
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IINTLSLFGFAVIMPMMFVDELGFTTSEWLQVWAAFFFTTIFS--
                                                                                                 ALAFCFAG-GVIAMISLRHVKT--PGHMHNLTPREKFAELSRAVTLLYTNRNIFLSSIVR
                                                                                                                                                       GSGAIAAAVMALLSDLTREQNRTKAMAFIGVSFGVTFAMA
                                                                                                                                                                                                                                                         LSQAIFQIPFGLLSDRI-GRKPMIIGGLL--VFALGSIIAALSDSIWGIIL----GRALQ 113
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                                                                                                                                                       ----MVLGPIVTHAF
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S.; Barrel
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RESULT 8
670042
multidrug-efflux transporter homolog yv C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision
C:Accession: G70042
R;Kunst, F.; Ogasawara, N.; Moszer, I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-388 <YOS>
A;Cross-references: GB:D90119; NID:g216974; PIDN:BAA14147.1; C;Superfamily: tetracycline resistance protein
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C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change
C;Accession: A37838
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J. Bacteriol. 172, 6942-6949, 1990
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                                                                                                                                                                GERQGFAGGLNSTFTSMGNFIGPLIAGALFDVHIEAPIYMAIGVSLAGVVIVLI
                                                                                                                                                                                                  PKHKGAAISVYNLSAGMSNFLAPAIAVVLL-----PWFSTIGVVIAYTALYLL
                                                                                                                                                                                                                                       KYFSELTFIAWSLLYSVVVLILLVFANGYWSIML--ISFVVFIGFDMIRPAITNYFSNIA
                                                                                                                                                                                                                                                                                                           VLSFGLSAFETLYSLYTADKVNYSPKDISIAITGGGIFGALFQIYFFD-----KFM
                                                                                                                                                                                                                                                                                                                                             INTLSLFGFAVIMPMMFVDELGFTTSE-WLQVWAAFFFTTIFSNIFWGIVAEKMGWMRVI
                                                                                                                                                                                                                                                                                                                                                                                GALGILAFIMSIVLIHDPKKSTTSGFQKLEPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFIVVIIHNVRSENSSSALGWYWAVYSVGIGVAGSYIPSFTIPIMGEMGTLWLALAFCFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPEGGTLADKLGKKLICIGLILESVSEEMEAV----GHNESVLMLSRVIGGMSAGMVMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKQIFVL-----YFNIFLIFLGIGLVIPVLPVYLKDLGLTGSDLGLLVAAFALSQMII 54
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                                                                                                                                                                                                                                                                        RWFGCLGMAASSLAF - - - YYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAV - - - FPALE
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20.5%;
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Pred. No. 1.1e-05
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   Albertini,
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     A.M.;
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C;Date: 13-Nov-1998 #sequence_revision C;Accession: E71614
R;Gardner, M.J. Tettelin, H.; Carucci, Pertea, M.; Salzberg, S.; Zhou, L.; Science 282, 1126-1132, 1998
A;Tille: Chromosome 2 sequence of the PA;Reference number: A71600; MUID:990217

Tettelin, H.; Carucci, alzberg, S.; Zhou, L.;

Sutton,

D.J.; Cummings, L.M.; Sutton, G.G.; Clayton,

Aravind, L.; R.; White, O

13-Nov-1998 #text_change 21-Jul-2000

2 sequence of the human A71600; MUID:99021743; F

n malaria parasite PMID:9804551

Plasmodium

falciparum 0.; membrane transporter PFB0465c - malaria C; Species: Plasmodium falciparum '

parasite

(Plasmodium

falciparum)

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C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauy, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Reference number: A69580; MUID:98044033; PMID:9384377

A:McCession: G70042
A:Status: prelininary, nucleic acid sequence not shown; translation not shown
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C;Superfamily: fosmidmycin resistance protein
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-444 < KUN>
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399
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                                                     LAPAIAVVLLPWFSTIGVVIAYTALYLLAFVL 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSAWVSGVVAEIITPQKTMLIGFVLWCVFHVLFLVFGLGQA----NYGLILLFYGIRGLAY
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ISSAL-----IGLISGYHTLFMILFAV 420
                                                                                                              LLSS--SHSVLFLMLSLILGGLASGVGLTSMQVSSLATVDPGMSGVASGIFSTFRYFGSI
                                                                                                                                                                                                                          FMTNQFGLNTSNSGMALSVFSIFMSASNWVGAQLHHKWGAKKII-FLSFAMMAGANLLFL
                                                                                                                                                                                                                                                                                                                ILLEVPLEFRREKRTQHPIIDFALFKSST--FTNANLSV----LLSNLMYAVLLIMPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLTPNSIATIRHVVSEKRLPKVFGFFG--LGAGLGAALGPFIGSILIDSFSWHSIFWVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLFLYSFIVVIIHNVRSENSSSALGWYWAVYSVGIGVA-GSYIPSFTIPIMGEMGTLWLA 178
                                                                                                                                                                 YMPOYFGHNYWMAMIPAI--ALGTFVAAFVPMAAVFPALEPKHKGAAISVYNLSAGMSNF
                                                                                                                                                                                                                                                                            MFVDELGETTSEWLQVWAAFFFTTIFSNIFWGIVAEKMGWMRVIRWFGCLGMAASSLAFY
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91; Conserv
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20.1%; Pred. No. 1.4e-05;
vative 87; Mismatches 185;
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RESULT 10
G64494
quinolone resistance protein norA homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Cate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: G64494
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Gl. rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus
A-Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                 A: Molecule type: DNA
A: Residues: 1-386 <BU
A: Cross-references: G
C: Genetics:
A: Map position: REV15
C: Superfamily: tetrac
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A:Status: preliminary; nucleic acid sequence not shown; translation not A:Status: preliminary; nucleic acid sequence not shown; translation not A:Molecule type: DNA
A:Residues: 1-457 <GAR>
A:Cross references: GB:AE001396; GB:AE001362; NID:g3845188; PIDN:AAC7188
A:Experimental source: clone 3D7
C:GenetLtcs:
A:Genet PFB0465c
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LIWGYIAIAVFMTGDGFELAFLSHYIKSLGFTPAEASFAFTLYGLAAALSAWVSGVVAEI
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                                         91;
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                                     Score 164.5; DB 2;
Pred. No. 5.6e-05;
1; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 168.5;
Pred. No. 3.
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                                                                                                                                                                               PIDN: AAB99579.1;
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                                                                                                                                                                             PID:g1592184;
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                                    NLSAGMSNFLAPATAVVLLPWFSTIGVVIAYTALYLLAFVLCAFIRVEQ 408
                                                                                                                                              ALYAINYNITISQVGFMIA----
                                                                                                                                                                                  VIMPMME - - - VDELGETTSEWLQVWAAFFFTTIFSNIF - - - WGIVAEKMGWMRVIRWFGC
                                                                                                                                                                                                                      ISYMKLEDIVENKN-KEKI-DVKKISTLFSFEFLKNRNFSSSFIINVSNVMINAGIYAYL
                                                                                                                                                                                                                                                                                                                               NVRSENSSSALGWYWAVYSVGIGVAGSYIPSFTIPIMGEMGTLWLALAFCFAGGVIAMIS 192
                                                                                                                                                                                                                                                                                                                                                                   YGKKFFIVCGTFFYGVSTLMYNFVSTVLG---FLIVRIFTGIFSAFVTPVAGSYIAAIAP
                                                                        IGIFIISFGMYLLSTSTTFLTILASLTIIAVGSSISSTATTSLAVKDIPTHRKGEAMGLF
                                                                                                          LGMAASSLAFYYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAVFPALEPKHKGAAISVY
                                                                                                                                                                                                                                                                                                                                                                                                       ITPQKTMLIGFVLWCVFHVL--FLVFGLGQANYGLILLFYGIRGLAYPLFLYSFIVVIIH 132
                                                                                                                                                                                                                                                                                             -LGEYMGIFNSAI-TLGFGIGPFIGGILADMYGIKMPFYFCGFLGILAAI-
                                                                                                                                              -----LTNILMALLQRSFGKLYDKLGNIMII-----
386
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th, T.; CONNECTON, P.
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001 |
Nature 413, 848-852, 2001 |
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s Дb õ В R;Parkhill, J.; Dougan, G.; James, R;Parkhill, J.; Connerton, P.; Cronin, A.; probable transporter STY1169 [imported] - Salmonella enterica subsp. enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 17-May-2002 AF0634 γQ D Qy 뫄 γQ δÃ A; Gene: STY1169 C; Superfamily: A; Molecule type: DNA A; Residues: 1-426 <P A; Cross-references: GB:AL513382; C; Accession: Matches Query Match Genetics 113 172 101 57 59 LAAALSAWVSGVVAEIITPQKTMLI------GFVLWCVFHVLFLV---FGL-----Local 1 MIAKFFPWYS----EITRPQKNALFSAWLGYVFDGFDFMLIFYIMYLIKADLGLTDMEGA STY1169 RFIVGMGMAGKYACASTYAVESWPKHLKSKASAFLVSGFGIGNIIAAYFMPSFAE-AYGW VYSVGIGVAGSY-----VTLLYTNRNIFLSSIVRIINTLSLFG----FAVIMPMMFVDELGFTTSEWLQVWAAFFFT LALAFCFAGGVIAMISLR-FLATAAFIGRPFGGALFGLLADKFGRK----PLMMWSIVAYSVGTGLSGLASGVIMLTLS RAAFFVGLLPVLLVIYIRARAPESKEWEEAKLSGLGKHSQSAWSVFSLSMKGLF-----99; Similarity Escherichia coli hypothetical protein Conservative <PAR> -GQANYGLILLFYGIRGLAYPLFLYSFIVVIIHNVRSENSSSALGWYWA :: 7.3%; <u>::</u> 66; Score 162.5; PIDN: CAD08257.1; Pred. Davis, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr Mismatches NO. 8.7e-05; HVKTPGHMHNLTPREKFAELSRA DB 2; 147; PID:g16502304; ----IPSFTIPIMGEMGTLW b4279 Indels Length 426; 131; GSPDB:GN00176 Gaps 217 112 148 56 273 171 176 100 17; serovar

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C;Accession: C70082
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C; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B; Capuano, V.; Carter, N.M.; Chc A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mueel Y. M.; Ogawa, K.; Ogivara, A.; Oudega, B.; Fark, S.H.; Parro, V.; Pohl, T.M.; Portetellé, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A: Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Scoffone Sequence of the Gram-positive bacterium Bacillus subtilis. A; Scoffone C70082
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A; Gene: yxlH
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C770082
multidrug-efflux transporter homolog yxlH - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: C70082
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A;Experimental source: strain 168
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les 93; Conservative
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AAATLSEVEL-RETSRIAYSVMLISEAVTGVCLLYVPELAALETVCITHACIGLALGEVE
                                                    AASSLAFYYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAA-------VF 344
                                                                                                                                                          GFAVIMPMMFVDELGFTTSEWLQVWAAFFFTTIFSNIFWGIVAEKMGWMRVIRWFGCLGM 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQKTMLI-GFVLWCVFHVLFLVFGLGQANYGLIL---LFYGIRGLAYPL--FLYSFIVVI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYIYVPVF-----SLYLEDLHFSYGAIGIILGSYGVTQILLRFPLGLLSDILFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYIAIAVEMTGDGFELAFLSHYIKSLGFTPAEASFAFTLYGLAAALSAWVSGVVAEII-T 76
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                                                                                                           GFT----PLYMNQLGMGDAELLWVMSAFF----
                                                                                                                                                                                                                 AGLVICCFIQDPSAPPANRGTIRVNQYIKDTLRLPKLKLFT----ILSMTAHAVLFITVF 239
                                                                                                                                                                                                                                                                  AGGVIAMISLRHVKTPGHMHNLTPREKFAELSRAVTL-LYTNRNIFLSSIVRIINTLSLF 242
                                                                                                                                                                                                                                                                                                                                                                             IHNVRSENSSSALG--WYWAVYS-----VGIGVAGSYIPSFTIPIMGEMGTLWLALAFCF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                    LRKQLLIAGFGFSVLSSLLFLMFD----SFFFVLAARLFAGITASTWVMATILYA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.3%; Score 161.5; DB 2; 21.5%; Pred. No. 9.7e-05; tive 70; Mismatches 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 400;
                                                                                                        -----LPH 267
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Qy Db	Qy Db	Qу	Qу	Оy	Qу	Db Qy	Qу	Оy	Query Best I Matche	Qy Qy Qy Qy Db Db Db C:Spec C:Spec C:Acce C:	
406 VEQPGFSS 413 	363AGMSNELAPAIAVVLLPWESTIGVVIAYTALYLLAFVLCAFIR 405	330 LGTEVAAFVPMAAVFPALEPKHKGAAISVYNLS	274 TIFSNIFWGIVAEKMGWNRVIRW-FGCLGMAASSLAFYYMPQYFGHNYWMAMIPAIA 329 	214 LSRAVTLLYTNRNIFLSSIVRINTLSLFGFAVIMPMMFVDELGFTTSEWLQVWAAFFFT 273 :::	162 PSFTIPIMGEMGTLMLALAFCFAGGVIAMISLRHVKTPGHMHNLTPREKFAE 213	118 AYPLFLYSFIVVIIHN-VRSENSSSALGWYWAVYSVGIGVAGSYI 161 	58 GLAAALSAWVSGVVAEIITPOKTMLIGFVLWCVFHVLELVFGLGOANVGLILLFYGIRGL 117 : : : :	1 MSRNNKQWLGLPLHLIWGYIATAVFWTGDGFELAFLSHYI-KSLGFTPAEASFAFTLY 57 	7.2%; Score 159.5; DB 2; Length 428; st Local Similarity 20.3%; Pred. No. 0.00015; ches 99; Conservative 73; Mismatches 173; Indels 143; Gaps 19;	15 PAL	

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A;Molecule type: DNA
A;Residues: 1-387 <STO>
A;Cross-references: GB:AE005176; PID:g12722970; PIDN:AAK04221.1;
A;Experimental source: strain IL1403
C;GenetLcs:
A;Gene: blt
A;Molecule type: DNA
A;Residues: 1-455 <STO>
A;Cross-references: GB:BA000008; NID:g8979037; PIDN:BAA98872.1; GSPDB:GN00142
A;Experimental source: Strain J138
C;Genetics:
                                                                                                                                                                                             R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia [A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: F86573
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                   hexosphosphate transport [imported] - Chlamydophila pneumoniae (strain J138) C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C:Accession: F86573
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C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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R;Bolotin, A.; Wincker, P.; M
Genome Res. 11, 731-753, 2001
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ASI 435
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Search completed: March 13, 2003, 16:56:04
Job time: 17.7417 secs

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                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97464425; PubMed-9324246;
Heuel H., Turgut S., Schmid K., Lengeler J.W.;
"Substrate recognition domains as revealed by a
the D-arabinitol and ribitol transporters from
pneumoniae.";
J. Bacteriol. 179:6014-6019(1997).
-i- SUBCELLULAR LOCATION: Integral membrane pro
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STRAIN=1033-5P14 / KAY2026;
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Bacteria; Proteobacteria;
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    SUBCELLULAR LOCATION: Integral membrane protein (Potential).
    SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. CSBX

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active hybrids between n Klebsiella

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STRAIN-1033-5p14 / KAY2026;
MEDLINE-97464425; PubMed-9324246;
Heuel H., Turgut S., Schmid K., Lengeler
"Substrate recognition domains as reveale
the D-arabinitol and ribitol transporters
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                                          Bacteriol. 179:6014-6019(1997)
              SUBCELLULAR SIMILARITY:
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This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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TIGRFAMS; TIGR00897; 2A0114
MSRNNKQWLGLPLHLIWGYIAIAVFMTGDGFELAFLSHYIKSLGFTPAEASFAFTLYGLA
                                      MSINNKQWLGLPLNLLWGYIAIAVFMTGDGFELAFLSHYIKALGFSPAEASFAFTLYGLA
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7; Mismatches 28;
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005390; 032056;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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"BofC encodes a putative forespore
sigma K checkpoint.";
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"A 17.8 kb segment in the spoVB-nadC region of the Bacillus
168 chromosome: sequencing and ruv operon identification.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
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STRAIN=168 / PY79;
MEDLINE=97177783; PubMed=9025289;
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                                                                                                            Gene 188:29-33(1997).
-!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                 Gomez M., Cutting S.M.;
"Identification of a new sigmaB-controlled gene,
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                                                                          DEVELOPMENTAL STAGE:
       SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. CSBX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003662; sub_transporter. pfam; PF00083; sugar_tr; 1. TIGRPAMS; TIGR00897; 2A0118; 1.
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P-TYLARYGYSVSEWLQIWGTLFFVNIVFNIIFGAVGDKLGWRNTVMWFGGVGCGIFTLA
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7 (POTENTIA
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RX MEDLINE-98044033; PubMed=9384377;

RA Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Brignell S.C., Bron S.,

RA Borriss R., Boursier L., Brans A., Bran M., Brignell S.C., Bron S.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Hilbert H., Holsappell S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Hilbert H., Holsappell S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kunano M.,

RA McDian N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Presecan E., Pujic P., Purnelle B., Roche B., Rose M., Sadaie Y.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Sato T., Scanlan E., Takagi T., Takahashi H., Takemaru K.,

RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Viari A., Wambutt R., Weeler E., Wedler H., Wassarotti A.,

RA Viari A., Wambutt R., Weeler E., Wedler H., Wassarotti A.,

RA Viari A., Wambutt R., Weeler E., Wedler H., Wassarotti A.,
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"Sequence analysis of the Bacilius subtilis chromosome region be
the terC and odhab loci cloned in a yeast artificial chromosome.
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                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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InterPro; IPR000849; GlpT_transporter
InterPro; IPR003662; sub_transporter.
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Science 282:754-759(1998).
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MEDLINE=99000809; PubMed=9784136;
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                                      YTGWRGAMFIPGIICIIMGFILIDRLR--DTPQSL-GLPAIEKFRKEEDAHPHEETTADI
                                                                              IMGEMGTLWLALAFCFAGGVIAMISLRHVKTPGHMHNLTPREKFAELSRAVTLLYTNRNI
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C L., Tatusov
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R.L., Zhao (
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tches 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quinolone resistance protein norA.
NORA OR SAV0695 OR SA0650 OR MW0657.
Staphylococcus aureus (strain Mu50 / ATCC
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P21191;
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           Biochem. Biophys. Res. Commun. 172:1028-1034(1990).
-!- FUNCTION: INVOLVED IN QUINOLONE RESISTANCE. MAY CONSTITUTE
MEMBRANE-ASSOCIATED ACTIVE EFFLUX PUMP OF HYDROPHILIC.QUINC
                                                MEDLINE=91058531; PubMed=2173911;
Ohshita Y., Hiramat'su K., Yokota T.;
A point mutation in norA gene is responsible resistance in Staphylococcus aureus.";
                                                                                                            SEQUENCE OF 230-388 STRAIN=209P;
                                                                                                                                                                                                                                                                   Yamamoto K., Hiramatsu K.; "Genome and virulence determinants of high virulence community-acquired MRSA.";
                                                                                                                                                                    aureus
                                                                                                                                                                                                                                                                                                         MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa
Nagai Y., Iwama N., Asano K., Naimi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillales; Staphylococcus
NCBI_TaxID=158878, 158879, 196620, 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus
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01-MAY-1991 (Rel. 18, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-91072245;
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"Nucleotide sequence and characterization
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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l. 172:6942-6949(1990)
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PubMed=11418146;
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Kuroda H., Cui
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InterPro; IPR003662; sub_transporter.
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                                                   GERQGFAGGLNSTFTSMGNFIGPLIAGALFDVHIEAPIYMAIGVSLAGVVIVLI
                                                                                 PKHKGAAISVYNLSAGMSNFLAPAIAVVLL-----PWFSTIGVVIAYTALYLL
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Nucleic Acids Res. 28:2311-2314(2000).
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EMBL; AE002171; AAF37968.1;
EMBL; AP002547; BAA98872.1;
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Kalman S., Mitchell W., Marathe R., Lammel C., Fan Golinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C.
                                                                                                                                                                                                                         TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license list-sib.ch).
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"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
"In PONCTION: TRANSPORT PROTEIN FOR SUGAR PHOSPHATE UPTAKE (BY
                                                                                                                                                                                                                                                                                                                                                                                                               CHLMU
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STRAIN-MoPn / Nigg;
MEDLINE-20150255; PubMed-10684935;
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update
xose phosphate transport protein.
ROT entry is copyright. It is produced through a collaboration
Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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20.7%;
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                                        Integral membrane
O THE SLC37A FAMILY
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Pred. No. 0.01;
4; Mismatches 160;
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                                       membrane protein (Potentia
37A FAMILY OF TRANSPORTERS.
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             a collaboration
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RESULT 9
MUCK_ACICA
ID MUCK_A
AC P94131
DT 30-MAY
DT 30-MAY
DT 15-JUN
DE Cis,ci
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30-MAY-2000 30-MAY-2000 15-JUN-2002 MUCK_ACICA P94131;

(Rel. 39, Created)
(Rel. 39, Last sequence up
(Rel. 41, Last annotation
onate transport protein.

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Cis, cis-muconate

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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport;
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                                                                                                                                                                                                   IMGEMGTLWLALAFCFAGGVIAMISLRHVKTPGHMHNLTPREKFAELSRAVTLLYTNRNI
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                                                                                        LEEEAERELSTKEILFTYVLSNKWLWFLSFASFFIYVVRMAVND---
                                                                                                                                                             FLSSIVRIINT-------LSLFGFAVIMPMMFVDELGFTTSEWLQVWAAFF
                                                                                                                                                                                                                                 QGWGWPPCARLLTHWY-----SKSERGTWWSVWSTSHNIGGALIPVLTGIAID
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 SGFTG--
                     AGMSNFLAPAIAVVLLPWFSTIGVVIAYTAL------
                                                           LAFYYMPQYFGHN---YMMAMIPAIALGTFVAAFVPMAAV-FPALEPKHKGAAISVYNLS
                                                                                                                                                                                     YAGWRGAMFIPGIICIIMGFILIDRLR -- DTPQSL-GLPAIEKFKKEDLSHPHEETTADI
                                            LLFSILGLWGTHDRSIWWADGAFLFIIGFFL--FGPQMMIGLAAAELSHKKAA----GTA
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Similarity 21.48;
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TIGR00881; 2A0104;
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                                                                                                                 -FTTIFSNI-----FWGIVAE-----
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-WFAYFGAAFAGYPLGKVAQDWGWHGFFVALLACALI 435
                                                                                                                                                                                                                                                                                                                                                                                                                       ME.
                                                                                                                                                                                                                                                                                                                                                                       73;
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Pred. No. 0.(
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POTENTIAL.
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                      YLLAFVLCAFI
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Best Local
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InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
TIGRFAMS; TIGR00895; 2A0115; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ability to grow source.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams P.A., Shaw L.E.; "mucK, a gene in Acinetobacter calcoaceticus ADP1 (BD413),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BD413 / ADP1;
MEDLINE-97440147; PubMed-9294455,
                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U87258; AAC27117.1; -
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59
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                                      w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
                                               SRNNKQWLG---LPLHLIWGYIAIAVFMTGDGFELAFLSHYIKSL----GFTPAEASF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: PROBABLE
                 AFTLYGLA--AALSAW-----VSGVVAEIITPQKTMLIGFVLWCVFHVLFLVFGLGQA
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sen the Swiss Institute of Bioinformatics and the EMBL
SFTLAGMAIGGIFGGWACDRFGRVRIVVISILT----
                                     SNNORSRIGSHTWKIAFLFAFLALLV----DGADLMLLSYSLNSIKAEFNLSTVEAGMLG
                                                                           110;
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                                                                                    Similarity
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                                                                                             7.18;
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CYTOPLASMIC (PO
11 (POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cis, cis-muconate as the
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                                                                                                                        12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
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5 (POTENTIA
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                                                                           Mismatches
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        RX KEDLINE-98044033; PubMed-9384377;
RX KEDLINE-98044033; PubMed-9384377;
RA KUNST F., Ogasawara N., Moszer I., Albertini A.M., Bloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Schionych J. Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Schlan B., Schleich S., Schroeter R., Scoffone F.,
Schlan B., Schleich S., Schroeter R., Scoffone F.,
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Schlan B., Schleich S., Schroeter R., Scoffone F.,
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Microbiology 142:3113-3123(1996).
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Miwa Y., Fujita Y.;
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MEDLINE=97124196; PubMed=8969509;
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NCBI_TaxID=1423;
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Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Viari A., Wambutt R., Wedler E., Wedler H., Wasumoto K., Yata K.,
Winters P., Wipat A., Yamanoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
The complete genome sequence of the Gram-positive bacterium Bacillus
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EMBL; Z99124; CAB15946.1;
SubtiList; BG11144; yxiO.
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-i- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-i- SIMILARITY: SOME, TO YEAST YCD8 AND S.POMBE SPAC2G11.13.
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                             LLAFVLCAFIRVEQPGFSSAPVTEK 419
                                                                                          PMAAVFPALEPK-HKGAAISVYNLSAGMSNFLAP---AIAVVLLPWFSTIGVVIAYTALY
                                                                                                                       IYGKLAERFTG-KTMLYVGIVIYMIVCVYAYFMETTL--DFWILAMLVATSQGGIQAL--
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O1-JAN-1990 (Rel. 13, Created)
O1-JAN-1990 (Rel. 13, Last sequence up
O1-OCT-1994 (Rel. 30, Last annotation
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-i- FUNCTION: RESISTANCE TO TETRACYCLINE BY AN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus.
NCBI_TaxID=1311;
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van der Lelie D., Bron S., Venema G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
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   YIHWSYLLLIPMITIITVPFLMKLLKKEVRIKGHFDIKGIILMSVGIVFFMLFTTSYSIS
                                                                  ---GSY---IPSFTI---
                                                                                                                                                                                         LILLFYGIRGLAYPLFLYSFIVVIIHNVRSENSSSALGWYWAVYSVGIGVA--
                                                                                                                                                                                                                                                         PASTNWVNTAFMLTFSIGTAVYGKLSDQLGIKRLLLFGIIINCFGSVIGFV----GHSFFS
                                                                                                                                                                                                                                                                                                                 PAEASFAFTLYGLAAALSAWVSGVVAEIITPQKTMLIGFVLWCVFHVLFLVFGLGQANYG
                                                                                                                              LLIMARFIQGAGAAAFPALVMVVVARYIPKENRGKAFGLIGSIVAMGEGVGPAIVGMIAH
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PR01036; TCR
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EMBL; AP005276; BAB98285.1
InterPro; IPR000060; BCCT
                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                  modified
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                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum Bacteria; Actinobacteria; I
                                                                                                                                                                                                                                                                                                                                                                                                             Glycine betaine transporter betP BETP OR CGL0892.
                                                                            TIGRFAMS;
                                                                                                 Pfam; PF02028; BCCT;
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-ATCC 13032
                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium.
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Actinobacteria (class); A
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Best Local S
Matches 105
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SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
STRAIN-97426617; PubMed-9278503;
MEDLINE-97426617; Plunkett G. III, Bloch / Plattner F.R., Plunkett G. III, Glasner J. (Glasner J. / Chatrick H./
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                              Blattner F.R., Plunkett G. III, Bloch C./
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
                                                                                                                                                                            Hypothetical transport
                                                                                                                                                                                       16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                      YAJR_ECOLI P77726;
           "The complete genome sequence of Science 277:1453-1474(1997);
                                                                                                                    NCBI_TaxID=562;
                                                                                                                                 Escherichia
                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                        Escherichia
                                                                                                                                                                  YAJR OR B0427.
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05; Conservative
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Pred. No. 0.09
70; Mismatches
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                                                   Bloch C.A., Perna N.1
sner J.D., Rode C.K.,
                                                                                                                                            subdivision; Enterobacteriaceae;
                      Escherichia coli K-12.";
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                                                       Mayhew
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                                                     Burland V.,
/hew G.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000149; AAC73530.1; ALT_INIT.
EMBL; U82664; AAB40183.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Complete prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Probable).
SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
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                                                                                                                                                                                                                   TIWVVPNSSTHVLNRESGMVKGSFSKVLAEPRLLKLNFGIMCLHIL------LMSTFVA
                                                                                                                                                                                                                                                                      TREQNRTKAMAFIGVSFGITFAIAMVLGPIITHK-LGLHALFWMIAILATTG-----IAL
                                                                                                                                                                                                                                                                                                   -RSENSSSALGWYWAVYSVGIGVAGSYIPSFTIPIMGEMGTLWLALAFCFAGGVIAMISL
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IPANIA
                         KALNIS
                                                    --TSQFLGVAIGGSLGGWINGMFDGQGVFLA--GAMLAAVWLTVASTMKEPPYVSSLRIE
                                                                           AGMSNFLAPATAVVLLPW----FSTIGVVIAYTALYLLAFVLCAFIRVEQPGFSSAPVTE
                                                                                                         IVLWNAQ - - - TQFWQLV - -
                                                                                                                                 AFYYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAVFPALEPK-----HKGAAISVYNLS
                                                                                                                                                               LPGQLAD-AGFPAAEHWKVYLATMLIAFGSVVPFIIYAEVKRKMKQVFVF-CVGLIVVAE
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23.0%;
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                                                                                                       -VGVQLFFVAFNLMEALLPSLISKESPAGYKGTAMGVYS--
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 454;
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Davis R.W.;
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RESULT
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LACLA
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p36574; Q9CHM6;
01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
 TRANSMEM
DOMAIN
                                                                                                        TRANSMEM
DOMAIN
                                                                                                                                                                                                                        InterPro; IPR000109; PTR2.
InterPro; IPR005279; PepH_
Pfam; PF00854; PTR2; 1.
                                                                                                                                                                                                                                                              EMBL; U05215; AAA20660.1; ALT_INIT. EMBL; AE006303; AAK04800.1; -. PIR; A53620; A53620;
                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry 36:6777-6785(1997).
-!- FUNCTION: PROTON-DEPENDENT UPTAKE OF DI- OR TRI-PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21235186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94209318; PubMed=8157671;
Hagting A., Kunji E.R.S., Leenhouts K.J., Poolman
"The di- and tripeptide transport protein of Lacto
new type of bacterial peptide transporter.";
J. Biol. Chem. 269:11391-11399(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Di-/tripeptide transporter DTPT OR LL0702.
                                                                                                                                                                                   PROSITE; PS01022; PTR2_1; PROSITE; PS01023; PTR2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97327493; PubMed=9184160;
Hagting A., van de Velde J., Poolman B., Konings W.N.;
"Membrane topology of the di-and tripeptide transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome
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                                                                                         TRANSMEM
                                                                                                                                  DOMAIN
                                                                                                                                             TRANSMEM
                                                                                                                                                                    Peptide transport;

    -!- SUBCELLULAR LOCATION: Integral membrane protein.
    -!- SIMILARITY: BELONGS TO THE PTR2 FAMILY OF TRANSPORTERS

                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis.
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                           DOMAIN
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                                                                TRANSMEM
                                                                               DOMAIN
                                                                                                                                                            DOMAIN
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yjdL_subl_fam;
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 CYTOPLASMIC
                         EXTRACELLULAR (PROBABLE)
                                      PROBABLE
                                                   CYTOPLASMIC
                                                                 PROBABLE
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RESULT 15
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ID G6PU_HUMAN
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                                                                                                                                                                                                                                                                                                                                         AMIPAIALGTEVAA----FVPMAAVEPALEPKHKGAAISVYNLSAGMSNELAPAI--AVV
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3; Conservative
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     Q9UNS4; 096016;
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G6PT1 OR G6PT.
Homo sapiens (luman).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
MEDLINE-98342107: PubMed-9675154;
Kure S., Suzuki Y., Matsubara Y.,
Isshiki G., Hoshida C., Izumi I.,
"Molecular analysis of glycogen st
                                                                                                                                                                                                                                                                                           "structure of the gene mutated in glycogen storage dis Gene 227:189-195(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99150335; PubMed-10026167;
Hiraiwa H., Pan C.-J., Lin B., Moses S.W.
"Inactivation of the glucose 6-phosphate
storage disease type lb.";
J. Biol. Chem. 274:5532-5536(1999).
                                                                                                                                                                                         Janecke A.R., Bosshard N.U., Ma
Burchell A., Bartram C.R., Jan
Molecular diagnosis of type in
Hum. Genet. 104:275-277(1999).
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND ALTERNATI
MEDLINE-9918010; PubMed-10023055
Gerin I., Velga-Da-Cunha M., Noel
"Structure of the gene mutated in
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
Li Y. van de Werve G.;
"Four different transcripts of putative glucose-6-phosphate translocase in human leukocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional prediction of the coding sequences of 9 by analysis of cDNA clones from human fetal liver."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM TISSUE=Liver;
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"Genomic structure of the human glucose 6-phosphate translocase gen-
and novel mutations in the gene of a Japanese patient with glycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerin I., Veiga-Da-Cunha M., Ach
van Schaftingen E.;
"Sequence of a putative glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Urinary bladder; MEDLINE-98088917; PubMed-9428641;
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Zhang Y., Liu M., He F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 storage disease type Ib."; |
Hum. Genet. 103:493-496(1998).
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), A MEDLINE-99072316; PubMed-9856496;
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Sakura N., N
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PROSITE; PS00942; GLPT; 1.
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InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
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disease lb.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 248:426-431(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kida Y., Matsubara Y., Narisawa
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TISSUE SPECIFICITY: MOSTLY EXPRESSED IN LIVER AND KIDNEY.
DISEASE: DEFECTS IN G6PT1 ARE THE CAUSE OF GLYCOGEN STORAGE
DISEASE IB (GSD-1B).
SIMILARITY: BELONGS TO THE SLC37A FAMILY OF TRANSPORTERS.
CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 128.
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L; AF110820; AAF37736.1; -.
L; Y17864; CCAA76898.1; -.
L; AF116864; AAD13111.1; JOINED.
L; AF116863; AAD13111.1; JOINED.
L; AF116863; AAD13111.1; JOINED.
L; BC002400; AAH02400.1; -.
L; BC003589; AAH02400.1; -.
L; BC003589; AAH03589.1; -.
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EW; HGNC:4061; G6PT1.
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SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential).
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Sear Job	Qy Db	Qу Дъ	Qy	Db Qy	Оy	Qy Db	Qy Db	Оу	Ma Ma	SQ	FT FT	F F F F T
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13, 2003	NFLAPAIAV SFLAG	VAA : LFRVTVTSD	MGWMRV : LVGSSYMSA	IVRIINTLS : ::: YLWVLST	LWLALAFCF 	NP,	AEIITPQ ::::: SDQMSARWL	GDGFELAFL	6.3%; 20.3%; vative	109 46360 MW;	339	118 149
2003, 16:53:47	AAISVYNLSAGMSNELAPAIAVVLLPWFSTIGVVIAYTALYLLAFVLCA 402 : :: :	WMAMIPAIALGTEVAAFVPMAAVEPALEPKHKG	IFWGIVAEKMGWMRVIRWFGCLGMAASSLAFYYMPQYFGHNY LIQEKGQSALVGSSYMSALEVGGLVGSIAAGYLSDRAMAKAGLSNYGNPRHGL	TLLYTNRNIFLSSIVRIINTLSLFGFAVIMPMMFVDELGFTTSEWLQVWAAFFFTTIFSN	IPIMGEMGTLWLALAFCFAGGVIAMISLRHVKTPGHMHNLTPREKFAELSRAV 	GLILLFYGIRGLAYPLFLYSFIVVIIHNVRSENSSSALGWYWAVYSVGIGVAGSYIPSFT	LAAALSAWVSGVVAEIITPQKTMLIGFVLWCVFHVLFLVFGLGQANY	WGYIAIAVFMTGDGFELAFLSHYIKSLGFTPAEASFAFTLYG	Score 140; DB 1; Length 429; Pred. No 0.11; 69; Mismatches 153; Indels 152;	/FIId=VAR_003185. L -> F (IN REF. 3). ; C0399332FE72694B CRC64;	/FTId=VAR_012356. G -> C (IN GSD-IB).	W -> R (IN GSD-IB). /FTId=VAR_007850. G -> E (IN GSD-IB). /FTId=VAR_003184. WIGGING / IN GSD-IB)
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Q9HWG1
Q8ZC53
Q53459
Q03325
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Q8ZQ32
Q8Z7M8
P94376
Q8ZPR3
Q8ZPG6
Q8Z716
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3232.531 Million cell updates/sec
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          Q9f415 escherichia
Q8zk49 salmonella
Q9hwg1 pseudomonas
Q8zc53 yersinia pe
Q53459 staphylococ
Q03325 staphylococ
Q03450 bacillus su
Q96186 plasmodium
Q58955 methanococc
Q8zq32 salmonella
Q8z7m8 salmonella
Q8zpr3 salmonella
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	Q8VU72	058638	Q8U4E5	Q9L134	Q98GA1	Q9X0F0	Q9PMS5	Q9ZF64	Q8Y7M4	Q979S3	Q93PW1	Q9FKV1	Q912B6	Q9RT59	Q99RC3	Q9HXP5	Q92CF5	Q9RTL7	Q8ZLE4	Q9K788	006473	Q9L8Q4	Q8Z257	066181	Q9ZNA9	P95885	Q9HRX5	Q9A129	Q9HWT2
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01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                      InterPro; IPR001064; Crystallin.
InterPro; IPR004748; Ketoglu.permease.
TIGR00897; ADD18; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SEQUENCE 424 AA; 46877 MW; BC7FEFDFC7A83962 CR
                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=C;
                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                          Ribitol transporter.
                                                                                                                                                                         Submitted (JUL-2000) to the EMBL/GenBank/DDBJ EMBL; AY005817; AAG01885.1; -:
                                                                                                                                                                                             "A non-antibiotic marker for amplification of plant transformation vectors in E. coli." _{i};
                                                                                                                                                                                                                  LaFayette P.R., Parrott W.A.;
                                                                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                        Escherichia coli
  61
                                        Similarity
                                                                                 Conservative
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Last sequence update)
Last annotation update)
                                                                                Score 2211; DB 2;
Pred. No. 4.4e-150;
; Mismatches 0;
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08ZK49;
01-MAR-2002 (TIEMBLIEL 2
01-MAR-2002 (TIEMBLIEL 2
01-JUN-2002 (TIEMBLIEL 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-LT2 / SGSC1412 / ATCC 700720;

MEDLINE-21534948; pubMed-11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W.,

COurtney L., Porwollik S., Ali J., Dante M., Du F., Hou

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., NY

Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
Hypothetical protein; Complete protect
SEQUENCE 408 AA; 44676 MW; DCE201
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STM4434.
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome
    190
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                                                                                  HNVRSENSSSALG--WYWAVYSVGIGVAGSYIPSFTIPIMGEMGTLWLALAFCFAGGVIA
                                                                                                                             VDVFGPKKVMVTGFIVYLLASVAFLNFALPSHDFGAILVTYMLRGVGYPLVCYSFLVRL-
                                                                                                                                                                     AEIITPQKTMLIGFVLWCVFHVLFLVFGLGQANYGLILLFYGIRGLAYPLFLYSFIVVII
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                                        -TIQLDNHQQGIGTSLFWVVYNLGFTIIGPVVAASLIPELGHINVMWAGMGVALL-GVLF
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Pred. No. 5.3e-37;
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DCE20DAAE075121B CRC64;
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M., Du F., Hou
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X MEDLINE-2043737; PubMed-10984043;

A Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., A Hickey M.J., Brinkman F.S.Y., Hufnagle W.O., Kowalik D.J., Lagrou M., A Hickey M.J., Brinkman F.S.Y., Hufnagle W.O., Kowalik D.J., Lagrou M., A Hickey M.J., Brinkman F.S.Y., Hufnagle W.O., Kowalik D.J., Lagrou M., A Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., A Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., A Smith K.A., Spencer D.H., Mong G.K.-S., Mu Z., Paulsen I.T., A Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

"Topportunistic pathogen.";

"Topportunistic pathogen.";

Nature 406:959-964 (2000).

"INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

"INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

"SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY."
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Best Local
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Pfam; PF00083; sugar_tr; 1.
Transmembrane; Complete proteome.
SEQUENCE 462 AA; 48818 MW; C2178D
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STRAIN=ATCC 15692
MEDLINE=20437337;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
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Bacteria; Proteobacteria;
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22.6%; | Pred. No. 2.7e-05;
Live 75; Mismatches 182
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MEDLINE-21470413; PubMed-11586360;

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Nature 413:523-527(2001).

TENDAIGE S. A. 1500-151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003662; sub_transporter.

Pfam; PF00083; sugar_tr; 1.

Hypothetical protebin; Complete proteome.

SEQUENCE 456 AA; 48790 MW; 74D65EF5495B4095 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8ZC53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yersinia pestis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=632;
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KQVFMGCVA-VLFIAEVVLWFA----
                                                       -NIFWGIVAEKMGWMRVIRWFGCLGMAASSLAFYYMPQYFGHNYWMAMIPAIALGTFVAA
                                                                                                                  CLHILLMSSF-VALPQMMAN-AGLAPA---QHWVVYLVTMLVSFAAVVPFIIYAEMKRRM
                                                                                                                                                                       IINTLSLEGEAVIMPMMFVDELGETTSEWLQVWAAFFFTTIFS-
                                                                                                                                                                                                                                  GLQALFWGIAILALLGIVITLTVVPSANSHVLNRESSMVKGSVSKVLHNSRLLKLNFGIM
                                                                                                                                                                                                                                                                                             ALAFCFAG-GVIAMISLRHVKT--PGHMHNLTPREKFAELSRAVTLLYTNRNIFLSSIVR
                                                                                                                                                                                                                                                                                                                                                                                                                   YPLFLYSFIVVIIHNV-RSENSSSALGWYWAVYSVGIGVAGSYIPSFTIPIMGEMGTLWL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSQAIFQIPFGLLSDRI-GRKPMIIGGLL--VFALGSIIAALSDSIWGIIL----GRALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAAALSAWVSGVVAEIITPOKTMLIGFVLWCVFHVLFLVFGLGQANYGLILLFYGIRGLA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAMNDNKMTPLELRATWGLGTVFSLRMLGMFMVLPVLTTYGMALSGASEALIGIAIGIYG
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 176; DB 16;
Pred. No. 6.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410
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-GQDLWI-IIAGVQL--FFIA
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RESULT
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Best Local
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Q53459;
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MEDLINE-94379790; PubMed-8092836;

Ng E.Y., Trucksis M., Hooper D.C.;

Ng E.Y., Trucksis M., Hooper D.C.;

"Quinolone resistance mediated by norA: physiologic characterization and relationship to flqB, a quinolone resistance locus on the staphylococcus aureus chromosome.";

Antimicrob. Agents Chemother. 38:1345-1355(1994).

--- SUBCELLUJAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

EMBL; S74031; AAB31949.1;
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InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
TIGRFAMS; TIGR00880; 2_A_01_02; 1.
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GERQGFAGGLNSTFTSMGNFIGPLIAGALFDVHIEAPIYMAIGVSLAGVVIVLI 375
                                                                                                                                                                                                               G--GVIAMIS---LRH---VKTPGHMHNLTPREKFAELSRAVTLLYTNRNIFLSSIV-RI 235
                                                                                                                                                                                                                                            GVTGLIADISPSHQKAKNFGYMSAIINSGF-ILGPGIGGFMAEVSHRM-----PFYFA
                                                                                                                                                                                                                                                             SFIVVIIHNVRSENSSSALGWYWAVYSVGIGVAGSYIPSFTIPIMGEMGTLWLALAFCFA
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                          PKHKGAAISVYNLSAGMSNFLAPAIAVVLL-----PWFSTIGVVIAYTALYLL
                                                          KYFSELTFIAWSLLYSVVVLILLVFANDYWSIML - - ISFVVFIGFDMIRPAITNYFSNIA
                                                                                       RWFGCLGMAASSLAF<sub>|</sub>---YYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAV---FPALE 348
                                                                                                                     VLSFGLSAFETLYSLYTADKVNYSPKDISIAITGGGIFGALFQIYFFD-----KFM
                                                                                                                                                   INTLSLFGFAVIMPMMFVDELGFTTSE-WLQVWAAFFFTTIFSNIFWGIVAEKMGWMRVI
                                                                                                                                                                                 GALGILAFIMSIVLIHDPKKSTTSGFQKLEPQ----
                                                                                                                                                                                                                                                                                                     SPEGGTLADKLGKKLIICIGLILESVSEEMFAV - - - - GHNESVLMLSRVIGGMSAGMVMP
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                                                                                                                                                                                                                                                                                                                                                                                                                          7.9%; Score 175; DB 2; Similarity 20.5%; Pred. No. 6.2e-05; 85; Conservative 77; Mismatches 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 01,
(TrEMBLrel. 01,
(TrEMBLrel. 21,
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Last sequence update)
Last annotation updat
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Q03325
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Q03325;
Q03325;
Q1-NOV-1996 (TrEMBLrel 01, 01-NOV-1996 (TrEMBLrel 21, 01-JUN-2002 (TrEMBLrel 21, FLUGROQUINOLONE resistance NORA1199(WT)).
Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aureus.";
Antimiorob. Agents Chemother. 37:1086-1094(1993).
-I- FUNCTION: INVOLVED IN FLUOROQUINOLONE RESISTANCE. MAY CONSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00083; sugar_tr; 1.
TIGREAMS; TIGR00880; 2_A_01_02; 1.
Transmembrane; Transport; Antibiot
SEOUENCE 388 AA; 42236 MW; 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSCRIPTION, AND NOT GENE AMPLIFICA BASIS FOR FLUOROQUINOLONE RESISTANCE EMBL; M80252; AAA16158.1; ... EMBL; M97199; AAA26658.1; ... InterPro; IPR004734; Drug_resist. InterPro; IPR003662; sub_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALLELE NORA 1199, SEQUENCE FROM N
STRAIN-SA-1199B, AND STRAIN-SA-1199B, PUBMED-8517696;
MEDLINE-93297926; PubMed-8517696;
KBBEZ G.W., Seo S.M., Ruble C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Efflux-mediated fluoroquinolone resistance in Staphylococcus
   263
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(P33449).

CAUTION: THE SEQUENCE SHOWN IS THE SAME FOR ALELLE CONTAINING ALL ALLELE NORAL199 (WILD TYPE). STRAIN SA-1199 CONTAINING ALL NORAL199 (WI) IS FLUOROQUINOLONE-SUSCEPTIBLE. INCREASED TRANSCRIPTION, AND NOT GENE AMPLIFICATION, OF NORAL199 I TRANSCRIPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN INDUCTION: FUNCTION OF NORAL199 PROTEIN AS MULTITRANSPORTER IS INHIBITED BY RESERPIN.
SIMILARITY: BELONGS TO THE PROKARYOTIC DRUG RESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO MULTIDRUG RESISTANCE PROTEIN FROM BACILLUS
MKYFSELTFIAWSLIYSVIVLVLLVIADGYWTIMV--ISFVVFIGFDMIRPAITNYFSNI
                                                                                                                      GALGILAFIMSIVLIHDPKKVSTNG-FQKLEPQ
                                                                                                                                                 G--GVIAMI-----SLRHVKTPGHMHNLTPREKFAELSRAVTLLYTNRNIFLSSIV-R
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                            IRWFGCLGMAASSLAF---YYMPQYFGHNYWMAMIPAIALGTFVAAFVPMAAV---FPAL
                                                         LVLSFGLSAFETLYSLYTADKVNYSPKDISIAITGGGIFGALFQIYFFD
                                                                                     IINTLSLFGFAVIMPMMFVDELGFTTSE-WLQVWAAFFFTTIFSNIFWGIVAEKNGWMRV
                                                                                                                                                                                                                                          SPFGGTLADKLGKKLIICIGLIL---FSVSEFMFAIGQ-NFLILMLSRVIGGMSAGMVMP
                                                                                                                                                                                                                                                                                                    NKQILVL-----YFNIFLIFLGIGLVIPVLPVYLKDLGLTGSDLGLLVAAFALSQMII
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21.0%; Pred. No. 7.3e-05;
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01, Last sequence update)
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nnce NORAll99 protein (ALELLE
                                                                                                                                                                                                                                                                                                                                                                                                                         Antibiotic resistance. MW; 81551490F77BD663 CRC64;
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Bourlist S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dušterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Glims S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga'k., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Koetter P., Kohingstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Miauno M., Moestl D., Nakai S., Noback M.,
RA Medina N., Mellado R.P., Miauno M., Moestl D., Nakai S., Noback M.,
RA Presecan E., Pujic P., Purnėlle B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegaer T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998
01-JAN-1998
01-MAR-2002
                                                                                                                                                                 Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
FOR SUBCELLULAR LOCATION: INTEGRAL MEMBANE PROTEIN (BY
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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                             Transmembrane;
                                                     InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1
                                                                                                                    EMBL;
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                                                                                   299122; CAB15538.1;
Pro; IPR003662; sub_
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                                                                                                                                               Science 282:1126-1132(1998).
EMBL; AE001396; AAC71882.1; -.
SEQUENCE 457 AA; 51861 MW;
                                                                                                                                                                                                    Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind I Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J., Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.; "Chromosome 2 sequence of the human malaria parasite Plasmodium"
                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa;
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HVL--FLVFGLGQANYGLILLFYGIR-----GLAYPLFLYSFIVVIIHNVRSENSSSALG
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                                       YVISYMKIIGCSDVKYKDSSWIYVLTLLFQCFFGFFGGILNQNLGPQISVLLGGWLMCLG
                                                                  FLSHYIKSLGFTPA···EASFAFTLYGLAAALSAWVSGVVAEIITPQKTMLIGFVLWCVF
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19.8%;
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Pred.
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Pred. No. 9e
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                                                                                                                                                  71DF3759109456FF CRC64;
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No. 0.00021
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Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S. M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
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01-JUN-1998
01-MAR-2002
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Q58955;
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-:- SUBCELLULAR LOCATION: IN
-:- SIMILARITY: TO THE DRUG
EMBL; U67596; AAB99579.1: -.
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-JAL-1 / DSM 2661 / ATCC 43067; MEDLINE-96337999; PubMed-8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanoo
Methanococcaceae; Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical MJ1560.
                                                                                                                                     Hypothetical
TRANSMEM
                                                                                                                                                                Pfam;
                                                                                                                                                                            InterPro;
                                                                                                                                                                                          TIGR; MJ1560;
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanococcus jannaschii
                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2190;
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                                                                                                                                                              PF00083;
                                                                                                                                                                           IPR003662; sub_transporter.
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3 (TrEMBLrel. 06,
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al protein MJ1560.
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                                                                                                                                                  protein;
                                                                                                                                                              sugar_tr;
  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanococci;
                                                                                                                                                                                                                                INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
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01-MAR-2002
01-JUN-2002
                                                                                                                                                                    InterPro; IPR003662; sub_transporter.

Pfam; PF00083; sugar_tr; 1.

Sugar transport; Hypothetical protein; Complete
SEQUENCE 426 AA; 46492 MW; F5E7C8D65FB33857
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-IT2 / SGSC1412 / ATCC 700720;
STRAIN-IT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
MCClelland M., Sanderson K.E., Spleth J., Clifton S.W.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., M
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nha
Ryaterston R., Wilson R.K.;
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SEQUENCE
                                                                                                                                                                                                                                                                                Nature 413:852-856(2001).
EMBL; AE008749; AAL20063.1; -.
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative sugar transport STM1132
                                                                                                                                                                                                                                                                                                                                                          'Complete genome sequence of Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=602;
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                            59 LAAALSAWVSGVVAEIITPQKTMLI---
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386 AA;
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gar transport protein.
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                                                                               68;
                                                                                                    Score 162.5; DB 16; Pred. No. 0.00053;
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S., Layman
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MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain in Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Churcher S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Frogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Krogh A., Earsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Krogh A., Stevens K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                       Pfam; PF00083; Sugar_tr; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 426 AA; 46546 MW: KREGEIDOCOMP.
                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of a enterica serovar Typhi CT18.";
Nature 413:848-852(2001). |
EMBL; AL627269; CAD08257.1; -.
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                      A Kunst F. Ogsawara N. Moszer I. Albertini A.M. Alloni G.
A Azevedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
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A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
A Chim K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Gallzzi A., Galleron N.,
A Gliseppi G., Guy B.J., Haga K., Haich J., Harwood C.R., Henaut A.,
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A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

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Microbiology 142:3113-3123(1996).
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Hypothetical protein yx
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Miwa Y., Fujita Y.;
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 Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
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Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
A Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
A Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
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Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
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Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
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Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the gram-positive bacterium Bacillus
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Submitted (NOV-1997) to the
EMBL: D83026; BAA11739.1; -.
EMBL; Z99123; CAB15890.1; -.
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(TTEMBLrel. 21, Last annotation update)
s family transport protein.
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Best Local S
Matches 97
                                                                                                                                                    Q8ZPG6 PRELLIPATION OF GRAPEGS;
Q8ZPG6;
Q1-MAR-2002 (TrEMBLrel. 20, Cr
01-MAR-2002 (TrEMBLrel. 21, Lr
01-JUN-2002 (TrEMBLrel. 21, Lr
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MEDLINE-21534948; PubMed-11577609;

MCCLELland M., Sanderson K.E., Spieth J., Clifton S.W., Latreill Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Laym Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
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Hypothetical protein; Complete protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protec
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Salmonella typhimurium.
Bacteria; Proteobacteria;
       NCBI_TaxID=602;
                                    Salmonella.
                                                                            Bacteria; Proteobacteria;
                                                                                                            Salmonella typhimurium
                                                                                                                                                STM1543
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EMBL; AE008759; AAL20285.
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InterPro; IPR003662; sub_tra
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-LT2 / SGSC1412 / ATCC 700720;
STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-116776609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreill Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Laym Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimum Complete genome sequence of Salmonella enterica serovar Typhimum C. Scott K. Salmonella enterica serovar Typhimum C. Scott K. Salmonella enterica serovar Typhimum C. Scott K. Salmonella enterica serovar Typhimum C. Scott K. Salmonella enterica serovar Typhimum C. Scott K. Salmonella enterica serovar Typhimum C. Scott K. Salmonella enterica serovar Typhimum C. Scott K. Salmonella enterica serovar Typhimum C. Scott K. Salmonella enterica serovar Typhimum C. Scott K. Salmonella enterica serovar Typhimum C. Scott K. Salmonella enterica serovar Typhimum C. Scott K. Sal
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NCBI_TaxID=601;
                                                            Bacteria; Proteobacteria;
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                                                                                                                       Membrane
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Hypothetical protein; Complete protesequence 428 AA; 46461 MW; 20901
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EMBL; AE008767; AAL20462.1;
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Best Local Similarity 20.3
Matches 99; Conservative
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Pfam; PF00083; sugar_tr; 1.
413 VKSKGFKA 420
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                                                                                                                                                                                                                                                                                                       202 -----FENHEDVILSDDGRATPSL---GYYMKQPMVWATTLAFFSYNYI----LFFFL 247
                                                                                                                                                                                                                                                                                                                                          214 LSRAVTLLYTNRNIFLSSIVRIINTLSLFGFAVIMPMMFVDELGFTTSEWLQVWAAFFFT 273
                                                                                                                                                                                                                                                                                                                                                                                  151 -----PI----VGLLALSLGWRPAFGIIFLFGLVWVLLWYFIVSDKPTMSKRLAPEERID- 201
                                                                                                                                                                                                                                                            274 TIFS---NIFWGIVAEKMGWMRVIRW-FGCLGMAASSLAFYYMPQYFGHNYWMAMIPAIA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 AYPLFLYSFIVV-------IIHN-VRSENSSSALGWYWAVYSVGIGVAGSYI 161
                                                                                                                                                                                                                                                                                                                                                                                                                       162 PSFTIPIMGEMGTLWLALAFCFAGGVIAMISLRHV-----KTPGHMHNLTPREKFAE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 VTGLWTMLIVRVLFGMAEGPVSAAGNKIINNWISRKESATAIGIFSAGSPLGGAVSG--- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 FIGYALFNFIDGWASDKVGPKTVFLIAALLWSV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 GLAAALSAWVSGVVAEIITPQKTMLIGFVLWCVFHVLFLVFGLGQANYGLILLFYGIRGL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKRKTMGWLIV-----FLLFIVYMLNYMDRSALSITAPLIEKELGFNAAEMGMIFSAF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSRNNKOWLGLPLHLIWGYIAIAVFMTG--DGFELAFLSHYI-KSLGFTPAEASEAFTLY 57
                                                                                                                                            LGVCLAGAAVCVAVSGTVST--TGSAITLMSVSLFLLYLTGPIYWAVIQDVVHKDKVGSV 362
                                                                                                                                                                                        LGTFVAAFVPMAAVFPALEPKHKGAAISVYNLS--
                                   VEOPGFSS 413
                                                                                                           -----AGMSNFLAPAIAVVLLPWFSTIGVVIAYTALYLLAFVLC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46519 MW; 5DBFE2EBD6E4AF74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.2%; Score 159.5; DB 16; Length 428; 20.3%; Pred. No. 0.00087; tive 73; Mismatches 173; Indels 143; Gaps
                                                                    -GFIVQFSGKYDYAFYLAGAIAIVSSLLVFVF 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -FCGLTGL
                                                                                                                                                                                        362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
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Search completed: March 13, 2003, 16:55:16 Job time: 31.0265 secs

